



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142047

To: Jeffrey Parkin
Location: rem/3d39/3c18
Art Unit: 1648
Friday, January 21, 2005

Case Serial Number: 10/085944

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

THIS PAGE BLANK (USPRO)

STIC-Biotech/ChemLib CKFZ

142-0477

From: 72607 Parkin, Jeffrey
Sent: Friday, January 07, 2005 9:05 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search for U.S. Serial No. 10/085,944

Would you please search SEQ ID NO.: 2 from the aforementioned application (U.S. Serial No. 10/085,944; Wang, W.) v. all relevant PUBLIC/COMMERCIAL databases.

Place results on PAPER.

-19-28

Please include the first 50 SUMMARIES.

Thanks!

JSP
AU 1648
REM 3D39
2-0908

119

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

STIC
 CM-1
 Pre-S

Vendors

IG
 STN
 Dialog
 APS
 Geninfo
 SDC
 DARC/Questel
 Other CGN

Type of Search

N.A. Sequence
 A.A. Sequence
 Structure
 Bibliographic

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 11:23:36 ; Search time 938 Seconds

(without alignments)
1411.633 Million Cell1 updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aataatgtctggaaacgccccggaaaaccgcgg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters:

9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : GenBmbl.*

1: 9b_ba:*

2: 9b_hhg:*

3: 9b_in:*

4: 9b_on:*

5: 9b_ov:*

6: 9b_dat:*

7: 9b_ph:*

8: 9b_pi:*

9: 9b_dr:*

10: 9b_ro:*

11: 9b_sts:*

12: 9b_sy:*

13: 9b_mn:*

14: 9b_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	28	100.0	342	14	FLD2CPM2	X51709	Dengue-2 vi
2	28	100.0	840	14	AF360860	AF360860	Dengue vi
3	28	100.0	840	14	AF360861	AF360861	Dengue vi
4	28	100.0	840	14	AF360862	AF360862	Dengue vi
5	28	100.0	840	14	AF360863	AF360863	Dengue vi
6	28	100.0	2319	14	S66064	S66064	structural
7	28	100.0	2325	14	AF469175	AF469175	Dengue vi
8	28	100.0	2325	14	AF469176	AF469176	Dengue vi
9	28	100.0	2325	14	AF509530	AF509530	Dengue vi
10	28	100.0	2325	14	AY04442	AY04442	Dengue vi
11	28	100.0	2357	6	AR232496	AR232496	Sequence
12	28	100.0	2357	14	DEN2NCG	D00146	Dengue virus
13	28	100.0	2469	14	DENJAMA	M15075	Dengue virus
14	28	100.0	2552	14	AY152336S1	AY152336S1	Dengue vi
15	28	100.0	2552	14	AY152040S1	AY152040S1	Dengue vi
16	28	100.0	2552	14	AY152044S1	AY152044S1	Dengue vi
17	28	100.0	2552	14	AY152048S1	AY152048S1	Dengue vi
18	28	100.0	2552	14	AY152052S1	AY152052S1	Dengue vi
19	28	100.0	2552	14	AY152056S1	AY152056S1	Dengue vi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	28	100.0	342	14	FLD2CPM2	X51709	Dengue-2 vi
2	28	100.0	840	14	AF360860	AF360860	Dengue vi
3	28	100.0	840	14	AF360861	AF360861	Dengue vi
4	28	100.0	840	14	AF360862	AF360862	Dengue vi
5	28	100.0	840	14	AF360863	AF360863	Dengue vi
6	28	100.0	2319	14	S66064	S66064	structural
7	28	100.0	2325	14	AF469175	AF469175	Dengue vi
8	28	100.0	2325	14	AF469176	AF469176	Dengue vi
9	28	100.0	2325	14	AF509530	AF509530	Dengue vi
10	28	100.0	2325	14	AY04442	AY04442	Dengue vi
11	28	100.0	2357	6	AR232496	AR232496	Sequence
12	28	100.0	2357	14	DEN2NCG	D00146	Dengue virus
13	28	100.0	2469	14	DENJAMA	M15075	Dengue virus
14	28	100.0	2552	14	AY152336S1	AY152336S1	Dengue vi
15	28	100.0	2552	14	AY152040S1	AY152040S1	Dengue vi
16	28	100.0	2552	14	AY152044S1	AY152044S1	Dengue vi
17	28	100.0	2552	14	AY152048S1	AY152048S1	Dengue vi
18	28	100.0	2552	14	AY152052S1	AY152052S1	Dengue vi
19	28	100.0	2552	14	AY152056S1	AY152056S1	Dengue vi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
FLD2CPM2
LOCUS FLD2CPM2
DEFINITION FLD2 CP2 virus RNA for capsid protein, partial, from a case of dengue shock syndrome (M2).
ACCESSION X51709
VERSION 1
KEYWORDS GI:59299
SOURCE capsid protein.
ORGANISM Dengue virus type 2
COMMENT viruses, ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 342)
AUTHORS Samuel,S., Koh,C.L., Pang,T., and Lam,S.K.
TITLE Nucleotide and encoded amino acid sequences of the capsid protein gene of three dengue-2 viruses isolated in Malaysia from patients with dengue haemorrhagic fever, dengue shock syndrome or dengue fever
JOURNAL Nucleic Acids Res. 18 (7), 1904 (1990)

JOURNAL MEDLINE 90245598
PUBMED 2336373
REFERENCE 1 (bases 1 to 342)
AUTHORS Koh,C.L.
TITLE Direct Submission
JOURNAL Department of Genetics and Cellular Biology, 510 Kuala Lumpur,
Malaysia
COMMENT See <X51708> and <M19197> for previously reported sequence. See <X51708> and <X5710> for capsid protein sequences of M1 and M3.
FEATURES Source
/organism="Dengue virus type 2"
/mol_type="genomic RNA"
/strain="M2", isolated from case of dengue shock syndrome
1. 342
/db_xref="taxon:11060"
1. ->342

CDS
/note="unnamed protein product; capsid protein, partial
/note="unnamed protein product; capsid protein, partial

(AA 1-114)"							
/codon_start=1							
/protein_id="CAA36005.1"							
/db_xref="GI:52300"							
/db_xref="GOA:Q89715"							
/db_xref="TREMBL:Q89715"							
KLEVALAFAFLRELTIPPIAGILKRWGTTIKSKAKAINVLGFRKEIGRMNLLNRRRTA							
GVIMLIPIITVA"							
ORIGIN							
Query Match	100.0%	Score 28;	DB 14;	Length 342;			
Best Local Similarity	100.0%	Pred. No.	0.15;				
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
Qy	1	AATATGGCTAACCGCAGAGAAACCCG	28				
Db	40	AATATGCTAACGCGAGAAACCCG	67				
RESULT 2							
LOCUS	AF160860	840 bp	ss-RNA	linear	VRL 11-FEB-2002		
DEFINITION	Dengue virus type 2 isolate LARD1432 polyprotein gene, Partial cds.						
VERSION	AF160860.1						
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970						
REFERENCE							
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,B.C. and Gould,E.A.						
TITLE							
JOURNAL							
MEDLINE	21571640						
PUBMED	11714970		</td				

TITLE	Molecular epidemiology of dengue type 2 virus in Venezuela: evidence for <i>in situ</i> virus evolution and recombination	CDS	/country="Venezuela" 1. .>840 /note="contains capsid, premembrane, and membrane proteins"
JOURNAL	J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)		
MEDLINE	21571640		
PUBMED	11714970		
REFERENCE	2 (bases 1 to 840)		
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,E.C. and Gould,E.A.		
JOURNAL	Submitted (15-MAR-2001) Flavivirus, CEB-Oxford, Mansfield Road, Oxford OX2 6UD, England		
FEATURES	Location/Qualifiers		
source	1. .>840 /organism="Dengue virus type 2" /mol type="genomic RNA" /isolate="LARD1910" /db_xref="taxon:11060"		
CDS	/country="Venezuela" 1. .>840 /note="contains capsid, premembrane, and membrane proteins" /codon_start=1 /product="polyprotein" /protein_id="AAI76290_1" /db_xref="GI:18644126" /translation="MNNQRKARSTPENMLKERNRVRSTVQQLTKRFSLGMLQGRGPL KLEMVALAFLRFLTIPPTAGILKEWGTICKSKAINVLGFRKEIGRMNLLRRRTA DITYKCPILRQNPEPDIDCWNCNSTSTWVYGTCTTGHRERRSVALPVHGMGLC TRTEFWMSSEGAWKHVORIETWLRLHPGFAIMAAILAYTIGTHFQKALIFILTAVA PSMT"		
ORIGIN			
Query Match	100.0%; Score 28; DB 14; Length 840;		
Best Local Similarity	100.0%; Pred. No. 0.14;		
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 AATATGCTGAACGGAGAAACCCG 28		
Db	40 AATATGCTGAACGGAGAAACCCG 67		
RESULT 6			
LOCUS	S66064		2319 bp DNA linear
DEFINITION	structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic, 2319 nt].		
Qy	1 AATATGCTGAACGGAGAAACCCG 28		
Db	40 AATATGCTGAACGGAGAAACCCG 67		
ORIGIN			
Query Match	100.0%; Score 28; DB 14; Length 840;		
Best Local Similarity	100.0%; Pred. No. 0.14;		
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 AATATGCTGAACGGAGAAACCCG 28		
Db	40 AATATGCTGAACGGAGAAACCCG 67		
RESULT 5			
LOCUS	AF360863		840 bp ss-RNA linear VRL 11-FEB-2002
DEFINITION	Dengue virus type 2 isolate LARD1996 polyprotein gene, partial cds.		
ACCESSION	AF360863		
VERSION	AF360863.1		
KEYWORDS	GI:18644127		
SOURCE			
ORGANISM			
REFERENCE	1 (bases 1 to 840)		
AUTHORS	Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,E.C. and Gould,E.A.		
JOURNAL	Submitted (15-MAR-2001) Flavivirus, CEB-Oxford, Mansfield Road, Oxford OX2 6UD, England		
FEATURES	Location/Qualifiers		
source	1. .>840 /organism="Dengue virus type 2" /mol type="genomic RNA" /isolate="LARD1996" /db_xref="taxon:11060"		
ORIGIN			

Query Match 100.0%; Score 28; DB 14; Length 2319;
 Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGCAGAGAACCGCG 28
 Db 37 AATATGCTGAAACCGCAGAGAACCGCG 64

RESULT 7
 AF469175 LOCUS AF469176 DEFINITION Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
 DEFINITION Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
 ACCESSION AF469176
 VERSION AF469176
 KEYWORDS Dengue virus type 2
 SOURCE ORGANISM ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 FLAVIVIRUS; Dengue virus group.
 1 (bases 1 to 2325)
 AUTHORS Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and Zhao, W.Z.
 TITLE Structural genes of dengue virus type 2 strain GD24/93 isolate from Nanhui, Guangdong, China
 JOURNAL Unpublished
 DIRECTOR 2 (bases 1 to 2325)
 AUTHORS Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and Zhao, W.Z.
 TITLE Structural genes of dengue virus type 2 strain GD24/93 isolate from Nanhui, Guangdong, China
 JOURNAL Unpublished
 REFERENCE 1 (bases 1 to 2325)
 AUTHORS Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and Zhao, W.Z.
 TITLE Structural genes of dengue virus type 2 strain GD24/93 isolate from Nanhui, Guangdong, China
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2325)
 AUTHORS Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and Zhao, W.Z.
 TITLE Direct Submission
 JOURNAL Submitted (16-JAN-2002) Department of Virology, The Military Medical Institute of Guangzhou Military District, Dong Guanzhuang Road 91, Guangzhou, Guangdong 510540, China
 FEATURES source
 /organism="Dengue virus type 2"
 /mol_type="genomic RNA"
 /strain="GD08/98"
 /db_xref="taxon:11060"
 /country="China: Nanhui, Guangdong Province"
 /note="Isolated from dengue haemorrhagic fever patient"
 <1..>225
 /note="contains structural C, M and E proteins"
 /codon_start=1
 /product="polyprotein"
 /protein_id="AAL9018_1"
 /protein_translation="MNNOQKAKTTPENMLKRERNRVSTVQQLTKRFSLGMLQGRGPLKLPMALYFLRFUTPPAGILKRWGTTIKSKAINVLRGFREIGRMNLTINRRREA
 GMNLIMLIFTVMMAFLHITTRNGEPMTIVSNCMCLSLKFTEDGVNMCTLMAMDLGELCE
 DITYKCEPLRNONEPEPDIDCMCNISTSWNTYCTGTCHEEKRVSALVPHVGMGE
 TRTEBTWNSBEGAWKHAORIETWLRLHFGFTIAILLLAYTIGHTFQLALIFILLTAYA
 PANTMRGIGISNRDFEVGGSGGSWDPVLESGSCVMTKPTFVMAKNSPDTLKEITKAOPA
 TURKYCEFAKLJNTNTTIESRCPIQGPESLKERDOKREVKHSTVDRGNGNGCCLPGKGG
 IIVTCAMFTCKNNBKGKTVOPENLEYTIVTPSPGEEFAIGNDIGHKREIKVTPQSSV
 SNWIKETLVTULKPNPAHKDKODVYVLSSEQGAHMTALTQGOMSGNLLFNGHILADTG
 LRMDLQDQKGSYSMCIGFKVVKVEATBQHGFTIVRQYBEDGSPCKIPEIMDIEK
 RYVLGRGLITVNPVTEKSDSPVNEAUVPGDGYLIICQVEPGOLKLMWKKGSSIGQF
 ETTMRGAKRMALIGDPAWDEGSLGQPSLQVQFQGKQHGVQFQGAIYGAASFQSVSTMKILG
 VIITWIGMNSRSTSLSVVLVGLVIVLYGVNVA"

ORIGIN AF509530 Query Match 100.0%; Score 28; DB 14; Length 2325;
 Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGCAGAGAACCGCG 28
 Db 40 AATATGCTGAAACCGCAGAGAACCGCG 67

RESULT 9
 AF509530 LOCUS AF509530 DEFINITION Dengue virus type 2 polyprotein gene, partial cds.
 DEFINITION Dengue virus type 2 polyprotein gene, partial cds.
 ACCESSION AF509530
 VERSION AF509530
 KEYWORDS Dengue virus type 2
 SOURCE ORGANISM ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 FLAVIVIRUS; Dengue virus group.

Query Match 100.0%; Score 28; DB 14; Length 2325;
 Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGCAGAGAACCGCG 28
 Db 40 AATATGCTGAAACCGCAGAGAACCGCG 67

RESULT 8

REFERENCE	AUTHORS	JOURNAL	FEATURES	source	Road, Oxford OX1 3SR, United Kingdom
1 (bases 1 to 2325) Ren, R., Yu, F., Dong, T., Wei, L., Hua, J., Yan, H. and Peng, C. isolation, identification and sequence analyses of dengue virus type 2 strain GD19/2001.	1. . 2325	1. . 2325	1. . 2325	1. . 2325	1. . 2325
Unpublished					
2 (bases 1 to 2325) Ren, R., Yu, F., Dong, T., Wei, L., Hua, J., Yan, H. and Peng, C. Direct Submission					
Submitted (05-MAY-2002) Microbiology Department, The Military Medical Institute of Guangzhou Military District, Dongguanzhuang Road, Guangzhou 510507, China					
Location/Qualifiers					
1. . 2325					
/organism="Dengue virus type 2"					
/mol_type="genomic RNA"					
/strain="GD19/2001"					
/specific_host="dengue fever patient"					
/country="China: Guangdong province"					
1. . >2325					
/codon_start=1					
/product="polyprotein"					
/protein_id="P354399.1"					
/db_xref="GI: 21070437"					
/translation="MNNRKQKARSTPPNMILKRENRNVRSTVQLTKRFSIGMLQRGRPL					
KLFMALVAFLRFLTIPPTAGLKLRRMNLNRRRTA					
GVIIMIPIPTAMAFHLLTRNGEPMIVGROEKSLIIFKTEDGYNMCTLMADIGELCE					
DITIYKCPPLQNEPEIDCWCNSNTSTWVYTCCTTGHRERKSVALPVHMGMLG					
TRTETWMSSSEGAWHYQRIETMILFILGFMAAATYKPTDFFELIKTEAKOPA					
TURKCYEAQCLNTTIESCRPQFGEPSLINEEQKRFCKHSMVDRGNGCGLGKGG					
IUTCAANFTCKENMEGVKVLPEPNLEYTGTGKHEEAVGNDTGKHGEKQFQSI					
IVTACELTYGTUTMECSPRTGLDIDNEMVNLQMBEKAALVHQWFDLPLWLGADTO					
SNWICKETLTENPKHAKQDQDVVLSQEGAHHTALTGELOMSGNLIFTGHLRK					
LRMDKLQKGMYSMTGKFKLKVKEAETQHQTIVYQEOEGDGSCKPCKPFEIMDLEK					
KLFRGLTQKMLTNPVNUEDTSPNIEAEPPGDSYII1GVEPGQKLKNWPKGSSSQM					
ETTMGAKRAKMAILGDTAWDFSGLGGVTSIGKALHQVFGAIYGAFAFSGSWTMKILIG					
VITWTGMNSRSRTSLSVSLVGVVTTLYLGAMVQA"					
ORIGIN					
100.0%; Score 28; DB 14; Length 2325;					
Best Local Similarity 100.0%; Pred. No. 0.14;					
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1 AATATGCTGAAACGCCAGAGAACCCGG 28					
Db 40 ATATGCTGAAACGCCAGAGAACCCGG 67					
RESULT 11					
AR232496					
LOCUS AR232496					
DEFINITION Sequence 1 from patent US 6455509.					
ACCESSION AR232496					
VERSION 1					
KEYWORDS GI:27274633					
SOURCE Unknown					
ORGANISM Unclassified					
REFERENCE 1 (bases 1 to 2357)					
AUTHORS Kochel, T.J., Porter, K.R., Raviprakash, K., Hoffman, S.L. and Hayes, C.G.					
TITLE Dengue nucleic acid vaccines that induce neutralizing antibodies					
JOURNAL Patent: US 6455509 1 24-SEP-2002;					
FEATURES Location/Qualifiers					
1. . 2357					
/organism="Unknown"					
/mol_type="genomic RNA"					
ORIGIN					
100.0%; Score 28; DB 6; Length 2357;					
Best Local Similarity 100.0%; Pred. No. 0.14;					
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1 AATATGCTGAAACGCCAGAGAACCCGG 28					
Db 40 ATATGCTGAAACGCCAGAGAACCCGG 67					
RESULT 10					
AY044442					
LOCUS AY044442					
DEFINITION 2325 bp ss-RNA					
ACCESSION VRL 10-FEB-2002					
VERSION AY044442					
KEYWORD AY044442.1 GI:18643733					
SOURCE Dengue virus type 2					
ORGANISM Dengue virus type 2					
Flavivirus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;					
Flavivirus; Dengue virus group.					
1 (bases 1 to 2325)					
Uzzategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R., , Holmes, E.C. and Gould, E.A.					
Molecular epidemiology of dengue type 2 virus in Venezuela:					
evidence for <i>in situ</i> virus evolution and recombination					
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)					
JOURNAL 21571640					
PUBMED 11714970					
REFERENCE 2 (bases 1 to 2325)					
AUTHORS Uzzategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.M., Holmes, E.C. and Gould, E.A.					
TITLE Direct Submission					
JOURNAL Submitted (09-JUL-2001) Flavivirus Group, CBER-Oxford, Mansfield					

TITLE	Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23350, San Juan 00931, Puerto Rico									
JOURNAL										
FEATURES										
source										
/organism="Dengue virus type 4"										
/note="contains core protein, matrix protein and envelope glycoprotein"										
/codon_start=1										
/product="polyprotein precursor"										
/protein_id="AAN38331_1"										
/db_xref="GI:28170840"										
/translation="MQRKCKVVRPPENMLKRRERNRVRSTPQGLVKRPFSTGLFSKGPKRLMVLAFITFLRVLSIPTAGILKRWGOKKNAIKLIGPREIGMLNLTNGRKSTI TLLCILPTWMAFHLSITPDGEMLNTSWKMGCRPLFEGINKCTLIAMDGEMCD TVTYKCPLLNTPEPDICWCMNLTSWKMGTQCGGERRSVSLPHSGMGBT RAETWNSSEGAKHQAVERSNWLRNFGFALLAGENAYMIGOTGICRTVFFVLMILYAP SYGRMCVGNGRDEVQGUSGAWDNDLWISQGKTSIDKEMAEHTGHITVVKVEGAGACKVPIBIRDKV LRTYCBEASISNITATPRCPQGPPLKEEDQPYICRDVDRGWNGGCLFGKGV EVKLDYDGETLTDCEBRSGIDDENMLMKKKTTWVHQWFLDLPWTAGADTESEV HWNKGERMVTFPVHAKRQDVTLVLSQEGAMHSALLAGATEVDSGDNHMFAHLCKV KVKIGRVSISSTMSGKFSLDKEMEAETGCTVVKYEGAGACKVPIBIRDYNE STYRGARRMALLGETAWDGSVGGIIFTSLGRKAHQVFGSYTTMFGVSWMIRLIGF LVLNWTQKXKFQFOPESPRLASAILNAHKDGVCGIRSTRLENMMQQTINELN"										
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 18
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY152052S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY152052
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 18
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY152052S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY152052
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 18
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY152048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY152048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	RESULT 17
Qy	1 AATATGCTGAACGGAGAACCGCG 28									AY15048S1
Db	37 AATATGCTGAACGGAGAACCGCG 64									AY15048
ORIGIN										
Query Match	100.0%	Score: 28;	DB: 14;	Length: 2552;						
Best Local Similarity	100.0%	Pred. No.: 0.13;								
Matches	28;	Conservative	0							

ORIGIN		Query Match	Score	DB	Length	
		Best Local Similarity	0.0%	0.13	2552	
		Matches	Conservative	Mismatches	Indels	Gaps
1	Y	AATATGCTTAAACGGAGAAAACGCCG	100.0%	0	0	0;
37	b	AATATGCTTAAACGGAGAAAACGCCG	100.0%	0	0	0;

source 1. .>2552
 /organism="Dengue virus type 4"
 /mol_type="genomic RNA"
 /isolate="D4_44_1998"
 /db_xref="taxon:110700"
 /country="Puerto Rico"
 /note="acronym: DEN-4"
 1. .>2552
 /note="contains core protein, matrix protein and envelope glycoprotein"
 /codon_start=1
 /product="polyprotein precursor"
 /protein_id="AAN33379_1"
 /db_xref="GI:2117939"
 /translation="MNQKVKVVRPPFNMLKRRNRVSTPQGLYKRFSTGLFGKGPLR
 MVLAFITLRLVMSLTPPTGILKRGOLKKNAKAKLIGFTRKEGRMLNLGRKRSTI
 TLLCLIPTMNPHLSPPATCQLKRNQQLKRNQQLKRNQQLKRNQQLKRNQQLKRNQQL
 TLLCLIPTMNPHLSPPATCQLKRNQQLKRNQQLKRNQQLKRNQQLKRNQQLKRNQQL
 RAYTKCPULLNTPEDEIDCWCNLTSTWMYGTCTOSGERRERKSVALTPHESOMGLET
 RAETWMSSSEGKHEAQRVESSLTLEPQDLAGMAYMAQGKPTLDFEJLKTTAKEVAL
 SYGNRCVGYNRDRVEGGAWTDVLIEHGCVTTMAQGKPTLDFEJLKTTAKEVAL
 LRTYCIEASISNLTATCTPCTPCTPCTPCTPCTPCTPCTPCTPCTPCTPCTPCTPCTP
 VTCARKFCSGKLTGKLTQLETFVWNGVATITPSPSV
 EVKLDYGEHLDCBPSGIDFENMILMKKTKWLVHKQWFLDLPLWNTAAGDTSEV
 HNNYKERMTFKVPHAKQDVTWLGSOEGAMHSALAGATEEVDSGDGHNMFAGLHKCKV
 RMELURIKGNSYIMCGKFS-IKREMAETQHGTVKVEGAPCKVPIERDVKE
 KVGRVISSTPLAINTNSVNTLEBPPRDSYLVIVGIVNSLTSIGKTAHOVESSVYTMTMEGVISWMMRILIG
 STYRGAKMAGMAILGETAWDGSGGELFTSIGKTAHOVESSVYTMTMEGVISWMMRILIG
 LVWITTEQYKFOPESPARLASATLNAAHKDVGCVGIRSTTLLENMWKOITNELLN"
 ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
 Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAAACCGCG 28
 Db 37 AATATGCTGAAACGGAGAGAAACCGCG 64

RESULT 29
 AY152096S1
 LOCUS VRL 29-SEP-2003
 DEFINITION Dengue virus type 4 D4.85_1994 polyprotein precursor, gene, partial
 ACCESSION AY152096
 VERSION AY152096.1
 KEYWORDS GI:28170941
 SEGMENT 1 of 4
 SOURCE Dengue virus type 4 (DEN-4)
 ORGANISM ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 REFERENCES 1 (bases 1 to 2552)
 AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vornam, V., Gubler, D.J. and McMillan, W.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
 FEATURES Location/Qualifiers 1..2552
 source 1..2552
 /organism="Dengue virus type 4"
 /mol_type="genomic RNA"
 /isolate="D4_113_1995VE"
 /db_xref="taxon:110700"
 /country="Venezuela"
 /note="acronym: DEN-4"
 CDS 1..2552
 /note="contains core protein, matrix protein and envelope glycoprotein"
 /codon_start=1
 /product="polyprotein precursor"
 /protein_id="AAN33383_1"
 /db_xref="GI:28170948"

/translation="MNQRKVKVVRPPENMLKRERNRVRSTPOGLVKRPSIGLFFGKGPLR
 MNLAFITFURVLSIPTTAGILKWRKGQLKQAKILIGFRMNLNGRKSRSTI
 TLLCLIPPTMFAHSTRUDEBPMNVAHKERGRPLFLKTTEGINKCTLIAMDGEMCED
 TAYTKCPLUVNTTPEBDICWCHNTSTWMYGTCAOSGERRRKRSVALTPHEGMGLET
 RAETWMSSEGAWKAQRVEWSLWRNPALLGEMATMIGQTKIQRIVTFVJMLVAP
 SYGNRCVGYNRDEVEGVGGANVDLLEHGCVTNAQGKPLDFTLTAKAVEVAL
 LRTYCIEASISINTTATCPTOEPYLITEEQDOOYICRRDVYDRGMENGCGFKGKGVY
 VTCRCKECSGSKITGQNLQLENLETTUTVNGDTAVGNDTSNHGHTATIPRSPSV
 EVKLPDGYGLTLDCPERSIDFENMILMKRKCTWLHQKFDLPLWAAAGADTSEV
 HWNKERKMTFKVPHARODVYTLVGSQSGAMHLAGALAGATEEVNSGDNHMFAGHLKCKV
 RMELKLKGMSYTMCSGRFSIKEMATOHGTTVVKYKEVGAACKVPIERDVRNCE
 KVGRVISSTPLAVENTSNTILEBPPGDSVTKYQVFSVYTMFGVSYMMRILIGF
 STYRGAKRMALGETAWDFGSVCGLETSLGKATHQVFSVYTMFGVSYMMRILIGF
 LUNWIGTNSRNTSMAMTCIAVGGTIAQGKPLDFTLTAKAVEVAL
 VHWIEQYKFPQPESPARLASALINAHKGVRGSRTRLENMWQQTNELN"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
 Best Local Similarity 100.0%; Pred. No. 0.13; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAAACCGCG 28
 Db 37 AATATGCTGAAACGGAGAGAAACCGCG 64

RESULT 30

AY152100\$1 LOCUS 2552 bp RNA linear VRL 29-SEP-2003
 DEFINITION Dengue virus type 4 D4.112_1995mQ polyprotein precursor, gene,
 partial cds.
 ACCESSION AY152100
 VERSION AY152100.1 GI:28170950
 KEYWORDS 1 of 4
 SEGMENT Dengue virus type 4 (DEN-4)
 SOURCE Dengue virus type 4
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Dengue virus group.

REFERENCE 1 (bases 1 to 2552)
 AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
 Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
 PUBLMED 12832629
 FEATURES source
 REFERENCE 2 (bases 1 to 2552)
 AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
 Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
 PUBLMED 12832629
 FEATURES source
 REFERENCE 1 (bases 1 to 2552)
 AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
 Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
 PUBLMED 12832629
 FEATURES source
 REFERENCE 1 (bases 1 to 2552)
 AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
 Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
 PUBLMED 12832629
 FEATURES source

REFERENCE 1 (bases 1 to 2552)
 AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
 Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
 PUBLMED 12832629
 FEATURES source

REF ID: AAN38391-1

/organism="Dengue virus type 4"
 /mol type="genomic RNA"
 /isolate="D4.112_1995mQ"
 /db_xref="taxon:11070"
 /note="acronym: DEN-4"
 /note="contains core protein, matrix protein and envelope
 glycoprotein"
 /codon_start=1

/product="polyprotein precursor"
 /protein_id="AAN38391-1"
 /db_xref="GI: 28170956"

/translation=MNQRKVKVVRPPENMLKRERNRVRSTPOGLVKRPSIGLFFGKGPLR
 MNLAFITFURVLSIPTTAGILKWRKGQLKRNKAKILIGFRMNLNGRKSRSTI
 TLLCLIPPTMFAHSTRUDEBPMNVAHKERGRPLFLKTTEGINKCTLIAMDGEMCED
 TAYTKCPLUVNTTPEBDICWCHNTSTWMYGTCAOSGERRRKRSVALTPHEGMGLET
 RAETWMSSEGAWKAQRVEWSLWRNPALLGEMATMIGQTKIQRIVTFVJMLVAP
 SYGNRCVGYNRDEVEGVGGANVDLLEHGCVTNAQGKPLDFTLTAKAVEVAL
 LRTYCIEASISINTTATCPTOEPYLITEEQDOOYICRRDVYDRGMENGCGFKGKGVY

/translation=MNQRKVKVVRPPENMLKRERNRVRSTPOGLVKRPSIGLFFGKGPLR
 MNLAFITFURVLSIPTTAGILKWRKGQLKRNKAKILIGFRMNLNGRKSRSTI
 TLLCLIPPTMFAHSTRUDEBPMNVAHKERGRPLFLKTTEGINKCTLIAMDGEMCED
 TAYTKCPLUVNTTPEBDICWCHNTSTWMYGTCAOSGERRRKRSVALTPHEGMGLET
 RAETWMSSEGAWKAQRVEWSLWRNPALLGEMATMIGQTKIQRIVTFVJMLVAP
 SYGNRCVGYNRDEVEGVGGANVDLLEHGCVTNAQGKPLDFTLTAKAVEVAL
 LRTYCIEASISINTTATCPTOEPYLITEEQDOOYICRRDVYDRGMENGCGFKGKGVY

WTCAKESSGSKITGKTNLVOIENLEYTVVTVHNGDTTHAVGNDTSNHGVAAATIPRSPSV
 EVKLPDYGEFLIDLCBPAKQDIDPMLKQFDTWLYKQWFLDPLWWTAGADTSEV
 HWNKERKMTFKVPHARQDVTYLGSOGAMHSALAGATEEVSDGDNHMFAGHLKCKV
 RMEKLRIKGMSYTMCSGRFSIKEMATOHGTTVVKYKEVGAACKVPIERDVRNCE
 KVGRVISSTPLAVENTSNTILEBPPGDSVTKYQVFSVYTMFGVSYMMRILIGF
 STYRGAKRMALGETAWDFGSVCGLETSLGKATHQVFSVYTMFGVSYMMRILIGF
 LUNWIGTNSRNTSMAMTCIAVGGTIAQGKPLDFTLTAKAVEVAL
 VHWIEQYKFPQPESPARLASALINAHKGVRGSRTRLENMWQQTNELN"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
 Best Local Similarity 100.0%; Pred. No. 0.13; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAAACCGCG 28
 Db 37 AATATGCTGAAACGGAGAGAAACCGCG 64

RESULT 31

AY152104\$1 LOCUS 2552 bp RNA linear VRL 29-SEP-2003
 DEFINITION Dengue virus type 4 D4.108_1996CR polyprotein precursor, gene,
 partial cds.
 ACCESSION AY152104
 VERSION AY152104.1 GI:28170959
 KEYWORDS 1 of 4
 SOURCE Dengue virus type 4 (DEN-4)
 ORGANISM Dengue virus group.

REFERENCE 1 (bases 1 to 2552)
 AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
 Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
 TITLE Selection-Driven Evolution of Emergent Dengue Virus
 JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
 PUBLMED 12832629
 FEATURES Location/Qualifiers
 1. .>2552
 /note="contains core protein, matrix protein and envelope
 glycoprotein"
 /codon_start=1
 /product="polyprotein precursor"
 /organism="Dengue virus type 4"
 /mol type="genomic RNA"
 /isolate="D4.112_1995mQ"
 /db_xref="taxon:11070"
 /note="acronym: DEN-4"
 /note="contains core protein, matrix protein and envelope
 glycoprotein"
 /codon_start=1

/product="polyprotein precursor"
 /protein_id="AAN38387_1"
 /db_xref="GI: 28170957"

/translation=MNQRKVKVVRPPENMLKRERNRVRSTPOGLVKRPSIGLFFGKGPLR
 MNLAFITFURVLSIPTTAGILKWRKGQLKRNKAKILIGFRMNLNGRKSRSTI
 TLLCLIPPTMFAHSTRUDEBPMNVAHKERGRPLFLKTTEGINKCTLIAMDGEMCED
 TAYTKCPLUVNTTPEBDICWCHNTSTWMYGTCAOSGERRRKRSVALTPHEGMGLET
 RAETWMSSEGAWKAQRVEWSLWRNPALLGEMATMIGQTKIQRIVTFVJMLVAP
 SYGNRCVGYNRDEVEGVGGANVDLLEHGCVTNAQGKPLDFTLTAKAVEVAL
 LUNWIGTNSRNTSMAMTCIAVGGTIAQGKPLDFTLTAKAVEVAL
 VHWIEQYKFPQPESPARLASALINAHKGVRGSRTRLENMWQQTNELN"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
 Best Local Similarity 100.0%; Pred. No. 0.13; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAAACCGCG 28
 Db 37 AATATGCTGAAACGGAGAGAAACCGCG 64

RESULT 32

AY152104\$1 LOCUS 2552 bp RNA linear VRL 29-SEP-2003

DEFINITION Dengue virus type 4 D4.108_1996CR polyprotein precursor, gene,
 partial cds.
 ACCESSION AY152104
 VERSION AY152104.1 GI:28170959
 KEYWORDS 1 of 4
 SOURCE Dengue virus type 4 (DEN-4)
 ORGANISM Dengue virus group.

REFERENCE 1 (bases 1 to 2552)

AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
 Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.

TITLE Direct Submission

JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
 Piedras, PO Box 23360, San Juan 00931, Puerto Rico

PUBLMED 12832629

FEATURES Location/Qualifiers

1. .>2552
 /note="contains core protein, matrix protein and envelope
 glycoprotein"
 /codon_start=1

/product="polyprotein precursor"
 /protein_id="AAN38387_1"
 /db_xref="GI: 28170957"

/translation=MNQRKVKVVRPPENMLKRERNRVRSTPOGLVKRPSIGLFFGKGPLR
 MNLAFITFURVLSIPTTAGILKWRKGQLKRNKAKILIGFRMNLNGRKSRSTI
 TLLCLIPPTMFAHSTRUDEBPMNVAHKERGRPLFLKTTEGINKCTLIAMDGEMCED
 TAYTKCPLUVNTTPEBDICWCHNTSTWMYGTCAOSGERRRKRSVALTPHEGMGLET
 RAETWMSSEGAWKAQRVEWSLWRNPALLGEMATMIGQTKIQRIVTFVJMLVAP
 SYGNRCVGYNRDEVEGVGGANVDLLEHGCVTNAQGKPLDFTLTAKAVEVAL
 LUNWIGTNSRNTSMAMTCIAVGGTIAQGKPLDFTLTAKAVEVAL
 VHWIEQYKFPQPESPARLASALINAHKGVRGSRTRLENMWQQTNELN"

LOCUS	AY152116S1	2552 bp	RNA	linear	VRL 29-SEP-2003	SOURCE	Dengue virus type 4 (DEN-4)
DEFINITION	Dengue virus type 4 D4.86_1994 polyprotein precursor, gene, partial cds.					ORGANISM	Dengue virus type 4 viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
ACCESSION	AY152116					REFERENCE	(bases 1 to 2552)
VERSION	AY152116.1					AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vormdam,V., Gubler,D.J. and McMillan,W.O.
KEYWORDS	i of 4					TITLE	Selection-Driven Evolution of Emergent Dengue Virus
SEGMENT	Dengue virus type 4 (DEN-4)					JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
SOURCE	Dengue virus type 4					PUBMED	12832629
ORGANISM	Dengue virus type 4					REFERENCE	(bases 1 to 2552)
	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;					AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vormdam,V., Gubler,D.J. and McMillan,W.O.
	Flavivirus; Dengue virus group.					TITLE	Direct Submission
REFERENCE	1 (bases 1 to 2552)					JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vormdam,V., Gubler,D.J. and McMillan,W.O.					FEATURES	Location/Qualifiers
TITLE	Selection-Driven Evolution of Emergent Dengue Virus					source	1. .2552
REFERENCE	1 (bases 1 to 2552)						/organism="Dengue virus type 4"
AUTHORS	Bennett,M., Vormdam,V., Gubler,D.J. and McMillan,W.O.						/mol_type="Genomic RNA"
TITLE	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico						/iso_id="D4-89-1994"
JOURNAL	Direct Submission						/db_xref="GI:28171002"
REFERENCE	1 (bases 1 to 2552)						/country="Puerto Rico"
AUTHORS	Bennett,M., Vormdam,V., Gubler,D.J. and McMillan,W.O.						/note="Acronym: DEN-4"
FEATURES	Location/Qualifiers						1. .>2552
source							/note="contains core protein, matrix protein and envelope glycoprotein".
							/codon_start=1
							/product="polypropeptide precursor"
							/protein_id="AAN34407_1"
							/translation="MNORKKVYVRPENMLKREERNRVRSTPOGLVKRFESTGLFSGKGPLR
							MVLAFITPLRVLSPTRGELPRMILKGRGLFLKTEINKCTLIAMDGEMCDE
							TLLCLIPPTMAFHLSSTRDEPLVIAVHERRGFLKTEINKCTLIAMDGEMCD
							TYVTKCPCLVNTPEPDIQWCHLTSSTMVYCTCOSERBRERCSVALPNSGMGLET
							RAETWMSGGAWKAQRYESWLLNPGFLLTQVTFVQVYKVGAPCKVPIERDVKE
							SYGNRCVGWNDRDEVEGSGGAVDYLVEHGGCVTMQAQKPLDFELTKTAKEVAL
							LRTYCIEASISINTATCPCPTOEPYKKEQDQYICPRDVNDRGENGCGIFGKGVY
							TCATKLGSGKTTQVNLQVQVATVQVQVATVQVQVATVQVQVATVQVQVATVQVQV
							EVKLDPGYELTDCEPRSDIDEMIUMKMKTTWIKOWFLDLPWTAGADTSEV
							HNNYKERMVTFKVPHAKRDVTVLGSODGKMSALAGATEEVNGDGHNMFMAGHLKCKV
							RMEKLRIKGMSTMCGKFSIDKEMAETQHGTWVQVYKVGAPCKVPIERDVKE
							KVYGRVISTSTPLAENTNEVNTLEPPPGDSITMIGCNSALTWHWRKGSTIGKMPF
							STYRGAKEMAILGCTAWDFGSGLFTSISGKAVHQSFGSVYTTMMEGVISMMRILIGP
							LWINGTNSRNTSAMTCIAGVQGTLFQPSGKLVQGKPLDFLTTTLEPPGDSKAVHQSFGSVYTTMMEGVISMMRILIGP
							VHTWTEQYKFOQESPALARASLNAHKDGVGTRSLTRLENMWKQTINELN"
ORIGIN							
						Query Match	100.0%
						Best Local Similarity	100.0%
						Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
						DEFINITION	Dengue virus type 4 (DEN-4)
						ORGANISM	Dengue virus type 4 viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
						REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vormdam,V., Gubler,D.J. and McMillan,W.O.
RESULT	35					LOCUS	AY152124S1
LOCUS	AY152120S1					DEFINITION	2552 bp RNA linear VRL 29-SEP-2003
DEFINITION	Dengue virus type 4 D4.89_1994 polyprotein precursor, gene, partial cds.					ORGANISM	Dengue virus type 4 viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
ACCESSION	AY152120					REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vormdam,V., Gubler,D.J. and McMillan,W.O.
VERSION	AY152120.1					AUTHORS	
KEYWORDS	i of 4						
SEGMENT							
Qy	1 AATATGCTGAAACGCCAGAGAAACCGCG 28						
Db	37 AATATGCTGAAACGCCAGAGAAACCGCG 64						
RESULT	36						
Qy	1 AATATGCTGAAACGCCAGAGAAACCGCG 28						
Db	37 AATATGCTGAAACGCCAGAGAAACCGCG 64						
RESULT	37						
LOCUS	AY152120S1						
DEFINITION	Dengue virus type 4 D4.89_1994 polyprotein precursor, gene, partial cds.						
ACCESSION	AY152120						
VERSION	AY152120.1						
KEYWORDS	i of 4						
SEGMENT							

RAETWMSSSEGAWHQAQRVESWILRNPGPALLAGPMAYMIGQKPIGLORTVFFVLMMLVAP
SYGRGRCVGNCNRDVEGGANWYDNLVLEHGCGVTTMAQKPTLDFELTAKTAKEVAL
ARTICLEASISNITATRCPQEPYLKEEQDQQYICCRDVUDRGNGCGLPGKGYY
EVKLKDYGELTDCBPRSGIDENMILMKMKCTWLVRKOMFELDPLPWTAGDTSEV
HMEKLKERMTPVKPHAKRQDVTVLGSOGAMHSALAGTEUDSGDGHMEEAGHLKCKV
KVVERVISSTPLAINTNSVNTIELEPPFDSDTIVYIVGIVSALATHWPKGSISIGKMP
STYTGAKRMALGTSWMTAWDGSGVGLFTSLGKAVHOVESVYTMMGCVISWMRILIG
LVWLTIGNTSNTSHAMTCAVGGTILFLGTFQADMGCVWSAGRELKGSGJFVVDN
VHTWTEQQKFQFPESPARLASATLNAAHKDRVCGTRSPTRLNNWWKRITNELN"

ORIGIN

Query Match Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Gaps 0;

RESULT 42
AY152148S1 LOCUS AY152148S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.83_1994 polyprotein precursor, gene, partial
cds
Db 37 AATATGTAAACGCCGAGAACCCGG 64

RESULT 43
AY152144S1 LOCUS AY152144S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.83_1994 polyprotein precursor, gene, partial
cde
Db 1 of 4
Accession AY152144
Version AY152144.1
Keywords Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beitran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Source Dengue virus type 4 (DEN-4)
Organism Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
Reference 1 (bases 1 to 2552)
Authors Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beitran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Title Selection-Driven Evolution of Emergent Dengue Virus - Rio
Journal Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PubMed 12832629
Reference 2 (bases 1 to 2552)
Authors Beitran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Title Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Journal Piedras, PO Box 23160, San Juan 00931, Puerto Rico
Features Location/Qualifiers 1. . 2552
Source /organism="Dengue virus type 4"
/mol type="genomic RNA"
/isolate="D4.83_1994"
/db_xref="taxon:11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
1. . >2552
/note="contains core protein, matrix protein and envelope
glycoprotein"
/codon_start=1
/product="polyprotein precursor"
/protein_id="AAAN38435_1"
/db_xref="GI: 28171065"
/translation="MNQRKKVVRPPFMKRRNRSVPQGLYKRFSTGKGKPLR
MVLAFITFLRVLSPPTAGLKRNQQLKRRNRSVPQGLYKRFSTGKGKPLR
TLLCLIPPTWAAHISSTRDPMLVAKHERRPLFEKTEGINKCTLIAMDLCMCE
TAYTKCPLLNTPEDDCWNLNTSTWNGTCAOSGERRERSVALPHSGMLET
RAETWMSSSEGAWHQAQRVESWILRNPGFALLVHNGCAGLMAYMQGQI
/translati0n="MNQRKKVVRPPFMKRRNRSVPQGLYKRFSTGKGKPLR
MVLAFITFLRVLSPPTAGLKRNQQLKRRNRSVPQGLYKRFSTGKGKPLR
TLLCLIPPTWAAHISSTRDPMLVAKHERRPLFEKTEGINKCTLIAMDLCMCE
TAYTKCPLLNTPEDDCWNLNTSTWNGTCAOSGERRERSVALPHSGMLET
RAETWMSSSEGAWHQAQRVESWILRNPGFALLVHNGCAGLMAYMQGQI
STYTGAKRMALGTSWMTAWDGSGVGLFTSLGKAVHOVESVYTMMGCVISWMRILIG
ARTICLEASISNITATRCPQEPYLKEEQDQQYICRDVUDRGNGCGLPGKGYY
EVKLKDYGELTDCBPRSGIDENMILMKMKCTWLVRKOMFELDPLPWTAGDTSEV
HMEKLKERMTPVKPHAKRQDVTVLGSOGAMHSALAGTEUDSGDGHMEEAGHLKCKV
KVVERVISSTPLAINTNSVNTIELEPPFDSDTIVYIVGIVSALATHWPKGSISIGKMP
STYTGAKRMALGTSWMTAWDGSGVGLFTSLGKAVHOVESVYTMMGCVISWMRILIG
LVWLTIGNTSNTSHAMTCAVGGTILFLGTFQADMGCVWSAGRELKGSGJFVVDN
VHTWTEQQKFQFPESPARLASATLNAAHKDRVCGTRSPTRLNNWWKRITNELN"

ORIGIN

Query Match Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 AATATGCTGAAACGCCGAGAACCCGG 28
Db 37 AATATGTAAACGCCGAGAACCCGG 64

RESULT 44
AY152148S1 LOCUS AY152148S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.81_1994 polyprotein precursor, gene, partial
cde
Db 1 of 4
Accession AY152148
Version AY152148.1
Keywords Dengue virus group.
Organism Dengue virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
Reference 1 (bases 1 to 2552)
Authors Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beitran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Title Selection-Driven Evolution of Emergent Dengue Virus - Rio
Journal Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PubMed 12832629
Reference 2 (bases 1 to 2552)
Authors Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beitran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Title Selection-Driven Evolution of Emergent Dengue Virus - Rio
Journal Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
Features Location/Qualifiers 1. . 2552
Source /organism="Dengue virus type 4"
/mol type="genomic RNA"
/isolate="D4.81_1994"
/db_xref="GI: 28171065"
/translation="MNQRKKVVRPPFMKRRNRSVPQGLYKRFSTGKGKPLR
MVLAFITFLRVLSPPTAGLKRNQQLKRRNRSVPQGLYKRFSTGKGKPLR
TLLCLIPPTWAAHISSTRDPMLVAKHERRPLFEKTEGINKCTLIAMDLCMCE
TAYTKCPLLNTPEDDCWNLNTSTWNGTCAOSGERRERSVALPHSGMLET
RAETWMSSSEGAWHQAQRVESWILRNPGFALLVHNGCAGLMAYMQGQI
/translati0n="MNQRKKVVRPPFMKRRNRSVPQGLYKRFSTGKGKPLR
MVLAFITFLRVLSPPTAGLKRNQQLKRRNRSVPQGLYKRFSTGKGKPLR
TLLCLIPPTWAAHISSTRDPMLVAKHERRPLFEKTEGINKCTLIAMDLCMCE
TAYTKCPLLNTPEDDCWNLNTSTWNGTCAOSGERRERSVALPHSGMLET
RAETWMSSSEGAWHQAQRVESWILRNPGFALLVHNGCAGLMAYMQGQI
STYTGAKRMALGTSWMTAWDGSGVGLFTSLGKAVHOVESVYTMMGCVISWMRILIG
ARTICLEASISNITATRCPQEPYLKEEQDQQYICRDVUDRGNGCGLPGKGYY
EVKLKDYGELTDCBPRSGIDENMILMKMKCTWLVRKOMFELDPLPWTAGDTSEV
HMEKLKERMTPVKPHAKRQDVTVLGSOGAMHSALAGTEUDSGDGHMEEAGHLKCKV
KVVERVISSTPLAINTNSVNTIELEPPFDSDTIVYIVGIVSALATHWPKGSISIGKMP
STYTGAKRMALGTSWMTAWDGSGVGLFTSLGKAVHOVESVYTMMGCVISWMRILIG
LVWLTIGNTSNTSHAMTCAVGGTILFLGTFQADMGCVWSAGRELKGSGJFVVDN
VHTWTEQQKFQFPESPARLASATLNAAHKDRVCGTRSPTRLNNWWKRITNELN"

ORIGIN

Query Match Score 28; DB 14; Length 2552;

Best Local Similarity 100.0% ; Pred. No. 0.13 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;	RESULT 44
Matches 28 ; Conservative 0 ;	AY152156S1
Qy 1 AATATGCTAACGCCAGAGAAACCGG 28	AY152156S1
Db 37 AATATGCTAACGCCAGAGAAACCGG 64	Dengue virus type 4 D4_79_1994 polyprotein precursor, gene, partial
DEFINITION	2552 bp RNA linear VRL 29-SEP-2003
ACCESSION AY152156	Accession AY152156
VERSION AY152156.1	GI : 28171076
KEYWORDS Flaviviridae;	
LOCUS 2552 bp	SEGMENT 1 of 4
DEFINITION Dengue virus type 4 D4_87_1994 polyprotein precursor, gene, partial	SOURCE Dengue virus type 4 (DEN-4)
ACCESSION AY152152	ORGANISM Dengue virus type 4
VERSION AY152152.1	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
KEYWORDS Flavivirus; Dengue virus group.	REFERENCES Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
SEGMENT 1 of 4	AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
SOURCE Dengue virus type 4	TITLE Selection-Driven Evolution of Emergent Dengue Virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;	JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
REFERENCE 1 (bases 1 to 2552)	PUBMED 12832629
AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.	FEATURES Location/Qualifiers
TITLE Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio	1. . >2552
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)	2. . >2552
REFERENCE 2 (bases 1 to 2552)	Source
AUTHORS Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.	/organism="Dengue virus type 4"
TITLE Direct Submission	/mol type="genomic RNA"
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio	/db_xref="D4_79_1994"
FEATURES Location/Qualifiers	/db_xref="taxon:11070"
1. . 2552	/country="Puerto Rico"
1. . >2552	/note="acronym: DEN-4"
Source	1. . >2552
/organism="Dengue virus type 4"	/note="contains core protein, matrix protein and envelope glycoprotein"
/mol type="genomic RNA"	/product="polypeptide precursor"
/db_xref="taxon:11070"	/protein_id="PAN18443_1"
/note="acronym: DEN-4"	/db_xref="GI: 28171083"
/note="contains core protein, matrix protein and envelope glycoprotein"	/translation="MNQRKVKVPPNMLKRERNRVSTPOGLVKRKFSTGLFSGKGPLR
/codon_start=1	MVLAFITPLRVLSIPTTAGILKNGOLKKNAKKLIGRKIGRMUNILNGRKSTI
/product="polypeptide precursor"	TLLCLIPITPAFHSTRUDEPLMIVAKHGRPLFKTEGINKCTLAMDGEMCD
/protein_id="PAN38439_1"	RAETWMSSEGAVKAQEVESWLNPMLKNGOLKKNAKKLIGRKIGRMUNILNGRKSTI
/db_xref="GI: 28171074"	SYGMRCKGMSYTMCSKFSIDKEMAFQHGTWVNGDTHAVGNDTSNHGVYATIPRSPEV
/translati on=MNQRKVKVPPNMLKRERNRVSTPOGLVKRKFSTGLFSGKGPLR	EVKLDYGEKLTIDCERSIDENMILMKMKTWVHKQWNLDPFLPWTAGADTSEY
MVLAFITPLRVLSIPTTAGILKNGOLKKNAKKLIGRKIGRMUNILNGRKSTI	HWNTRKDVNTKPVPHAKRQDVTVLGSOGAMESSALAGATEVDGDGHMEAGHLRKCV
TLLCLIPITPAFHSTRUDEPLMIVAKHGRPLFKTEGINKCTLAMDGEMCD	KVYGRVTSSTPLAENTNSVNIELEPPFGDSVYVIGNSALTWHFRKGSSIGKME
RAETWMSSEGAVKAQEVESWLNPMLKNGOLKKNAKKLIGRKIGRMUNILNGRKSTI	SPYRGAKMAGLGETAQDGSVGLFTSLGRAHVQFSGSVTTMFEGSVWMRILIGF
SYGMRCKGMSYTMCSKFSIDKEMAFQHGTWVNGDTHAVGNDTSNHGVYATIPRSPEV	LVLWIGTNSRNTSMANTCIAVGGTILFLGFTVQADNGCCVSMSGRELKCGSGIFVWDN
VTCAKFELSGSKTKISGNLYQOENLEYTVVWVNGDTHAVGNDTSNHGVYATIPRSPEV	VHTWTEQQKFQPSPARLASALINAHKGVCIRS1TRLENVWWKQ1TNELN"
EVKLPDGYLTIDCERPSGIDNEMLMKKGTWVQWFLDPLWTAGADTSEY	ORIGIN
HWNTRKDVNTKPVPHAKRQDVTVLGSOGAMESSALAGATEVDGDGHMEAGHLRKCV	Query Match 100.0% ; Score 28 ; DB 14 ; Length 2552 ;
RMPKLRIKGMSTMCMSGFSIDKEMAFQHGTWVNGDTHAVGNDTSNHGVYATIPRSPEV	Best Local Similarity 100.0% ; Pred. No. 0.13 ;
KVYGRVTSSTPLAENTNSVNIELEPPFGDSVYVIGNSALTWHFRKGSSIGKME	Mismatches 0 ; Mi matches 0 ; Indels 0 ; Gaps 0 ;
LVLWIGTNSRNTSMANTCIAVGGTILFLGFTVQADNGCCVSMSGRELKCGSGIFVWDN	DEFINITION Dengue virus type 4 D4_37_1992 polyprotein precursor, gene, partial
VHTWTEQQKFQPSPARLASALINAHKGVCIRS1TRLENVWWKQ1TNELN"	ACCESSION AY15216051
ORIGIN	1 AATATGCTAACGCCAGAGAAACCGCG 28
Query Match 100.0% ; Score 28 ; DB 14 ; Length 2552 ;	Db 37 AATATGCTAACGCCAGAGAAACCGCG 64
Best Local Similarity 100.0% ; Pred. No. 0.13 ;	
Matches 28 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;	
Qy 1 AATATGCTAACGCCAGAGAAACCGCG 28	DEFINITION Dengue virus type 4 D4_37_1992 polyprotein precursor, gene, partial
Db 37 AATATGCTAACGCCAGAGAAACCGCG 64	ACCESSION AY152161

VERSION KEYWORDS SEGMENT SOURCE ORGANISM	AY152160.1 1 of 4 Dengue virus type 4 (DEN-4) Dengue virus type 4 Flaviviridae; Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flaviviridae; Dengue virus group.	REFERENCE AUTHORS TITLE JOURNAL PUBLMED	1 (bases 1 to 2552) Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorniam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
REFERENCE AUTHORS TITLE JOURNAL PUBLMED	REFERENCE AUTHORS TITLE JOURNAL PUBLMED	2 (bases 1 to 2552) Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorniam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico Location/Qualifiers Location/Qualifiers	2 (bases 1 to 2552) Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorniam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico Location/Qualifiers Location/Qualifiers
REFERENCE AUTHORS TITLE JOURNAL PUBLMED	REFERENCE AUTHORS TITLE JOURNAL PUBLMED	CDS source /organism="Dengue virus type 4" /mol_type="genomic RNA" /isolate="D4_37_1992" /db_xref="taxon:11070" /country="Puerto Rico" /note="acronym: DEN-4" 1..>2552 /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="PAN38447.1" /db_xref="GI:28117101" /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="PAN38447.1" /db_xref="GI:28117102" /translation="MNQRKVKVVRPFENMLKRERNRVRSTFQGLYRKRFSTLFSERGPLR MVLAFITPLRVLSIPTTAAKIKRNGQLKNAKNAKIAKILIGERKEGRMLNILNGRKRTSI TLLCILPTMAFHLSSTRGEPELMIVKCHERPRRPLKFETINKCTLIAMDGEMCDE TVTYKOPLLNVNTEPIDCWNLSTWTVWGTCTYQSGERREKRKSVALPHSGNGLET RAETPMSSREGAWKAHQRTSNTLWRNPGLAAGMAYMRHTGQIORTYEFVNMMLVAP KVGRLRIGMSYTCMSGFPSIDEKMAETQHGTIVVVKYEGAGACKVIEIRDVNKE SYGRBCGCGNDRFVEFCYSCSNWPLLEHGGCUTTMQKPLDELTKTAKEVAL LRTYCJEAISNINITATRCPTQGBPLKEBQDQYICRSDVDRGWNCGGLPGGGV EVKLPDYGEITLCEPMSGDIDNEMKMKKTTWLUKQWFLDLPEWTAGADTSEV HWNYTKERMTVFKVPAKQDVTVLGQEGAMHSALAGATEVDSDGNMFAGHLKCKV RMEKLRIKGMSYTCMSGFPSIDEKMAETQHGTIVVVKYEGAGACKVIEIRDVNKE SYTRGAKRMLGETAWDFCSVGGLFTSLSKAVHQQFSGVYTMMFGYWSMMLIGFE LVLWGNITNSNTSNAMTCIAVGGITLFLGFTVOADMGCYVWSGRELKGSGIFVVVDN VHTWTQEKFQFQESPALARASALNAHKDGVCGIRSTTRLENVWKQITNELN"	CDS source /organism="Dengue virus type 4" /mol_type="genomic RNA" /isolate="D4_37_1992" /db_xref="taxon:11070" /country="Puerto Rico" /note="acronym: DEN-4" 1..>2552 /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="PAN38447.1" /db_xref="GI:28117101" /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="PAN38447.1" /db_xref="GI:28117102" /translation="MNQRKVKVVRPFENMLKRERNRVRSTFQGLYRKRFSTLFSERGPLR MVLAFITPLRVLSIPTTAAKIKRNGQLKNAKNAKIAKILIGERKEGRMLNILNGRKRTSI TLLCILPTMAFHLSSTRGEPELMIVKCHERPRRPLKFETINKCTLIAMDGEMCDE TVTYKOPLLNVNTEPIDCWNLSTWTVWGTCTYQSGERREKRKSVALPHSGNGLET RAETPMSSREGAWKAHQRTSNTLWRNPGLAAGMAYMRHTGQIORTYEFVNMMLVAP KVGRLRIGMSYTCMSGFPSIDEKMAETQHGTIVVVKYEGAGACKVIEIRDVNKE SYGRBCGCGNDRFVEFCYSCSNWPLLEHGGCUTTMQKPLDELTKTAKEVAL LRTYCJEAISNINITATRCPTQGBPLKEBQDQYICRSDVDRGWNCGGLPGGGV EVKLPDYGEITLCEPMSGDIDNEMKMKKTTWLUKQWFLDLPEWTAGADTSEV HWNYTKERMTVFKVPAKQDVTVLGQEGAMHSALAGATEVDSDGNMFAGHLKCKV RMEKLRIKGMSYTCMSGFPSIDEKMAETQHGTIVVVKYEGAGACKVIEIRDVNKE SYTRGAKRMLGETAWDFCSVGGLFTSLSKAVHQQFSGVYTMMFGYWSMMLIGFE LVLWGNITNSNTSNAMTCIAVGGITLFLGFTVOADMGCYVWSGRELKGSGIFVVVDN VHTWTQEKFQFQESPALARASALNAHKDGVCGIRSTTRLENVWKQITNELN"
REFERENCE KEYWORDS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SEGMENT SOURCE ORGANISM	ORIGIN Query Match Best Local Similarity 100.0%; Score 28; DB 14; Length 2552; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RESULT 46 AY152164S1 LOCUS AY152164S1 DEFINITION Dengue virus type 4 D4_25_1992 polyprotein precursor, gene, partial cds. ACCESSION AY152164 VERSION AY152164.1 KEYWORDS 1 of 4 SEGMENT Dengue virus type 4 (DEN-4) SOURCE Dengue virus type 4 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;	ORIGIN Query Match Best Local Similarity 100.0%; Score 28; DB 14; Length 2552; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RESULT 47 AY152168S1 LOCUS AY152168S1 DEFINITION Dengue virus type 4 D4_30_1992 polyprotein precursor, gene, partial cds. ACCESSION AY152168 VERSION AY152168.1 KEYWORDS 1 of 4 ORGANISM Dengue virus type 4 (DEN-4) VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.	ORIGIN Query Match Best Local Similarity 100.0%; Score 28; DB 14; Length 2552; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RESULT 48 AY152164S1 LOCUS AY152164S1 DEFINITION Dengue virus type 4 D4_25_1992 polyprotein precursor, gene, partial ACCESSION AY152164 VERSION AY152164.1 KEYWORDS 1 of 4 SEGMENT Dengue virus type 4 (DEN-4) SOURCE Dengue virus type 4 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

AUTHORS	Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
TITLE	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES	
Source	
	/note= "Dengue virus type 4" /mol_type="genomic RNA" /isolate="D4_30_1992" /db_xref="taxon:11070" /country="Puerto Rico" /note="acronym: DEN-4" 1..2552 /note="contains core protein, matrix protein and envelope glycoprotein" /organism="Dengue virus type 4" /codon_start=1 /product="polyprotein precursor" /protein_id="AN38455_1" /db_xref="GI:28171110" /translation="MNQQRKVVPRPFNNLKRKEFERNRVSTPQGLVYKRFSTGFLFGSGKPLR MVLAFITPLRVLSPPTAGILKPKRKKAKTAKLIGCFRKEMNLTNGRKSTI TLLCLIPPTMAGHFLSTRDGEPMIVAKERGKPLKETTEGINKCFLIAMDGEMCD TIVTKCPPLVNTEBDLWCNLNTSTWVYGTCTQSGERRRRSVALTPHESGTGLET RAETWMSSEGAWKAHQRTESWLNRPGFALLAGMAYGOTGIQRTVFKYEGAGAPCKPIERDVNE SYGMRCVGNGRDVEVGSGANDVLEHGCVTTMAQGPPLDDELTTKTAKEVAL LRTYCEASISNTTATRCPGPYPKREQDQYICRQDVRGNGCGFGKGKV VTCAKFSCSGKIKTENLVOLENTEYVUHNGDTHAQNHDGVTSPRSPEV EVKLPLDGYELTDCEPGRSLIDPNEMILMKMKCWTIYHKOMFLDLPLWTAGADTSEV HWNYKERMVTFKPHAKRQDVTWVGSAMHSALAGATEVGDGHNMFAGHLKCKV RMEKLRIKGMSYTMCSGRPSIDKEMAEOTQHGTIVKVEGAGAPCKPIERDVNE KVYGRVVISSTPLAENTNSVTNTEBLEPPGDSYIVIGVNSALAGATEVGDGHNMFAGHLKCKV STYRGAKRNAILGTADEGSVGLFTSGKAVHQHQSFSVYTMTGEVSWMRILIGF LVWIGTNSRNTSNAMTCIAVGGTILFLGFTVADMGCYVVSNSRELKCGS1FVVDN VHTWTEQYKFQFOPESPRLASALINAHKGVCVGRSTTRLENMWKOITNELN"
CDS	
	/note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="AN38455_1" /db_xref="GI:28171110" /translation="MNQQRKVVPRPFNNLKRKEFERNRVSTPQGLVYKRFSTGFLFGSGKPLR MVLAFITPLRVLSPPTAGILKPKRKKAKTAKLIGCFRKEMNLTNGRKSTI TLLCLIPPTMAGHFLSTRDGEPMIVAKERGKPLKETTEGINKCFLIAMDGEMCD TIVTKCPPLVNTEBDLWCNLNTSTWVYGTCTQSGERRRRSVALTPHESGTGLET RAETWMSSEGAWKAHQRTESWLNRPGFALLAGMAYGOTGIQRTVFKYEGAGAPCKPIERDVNE SYGMRCVGNGRDVEVGSGANDVLEHGCVTTMAQGPPLDDELTTKTAKEVAL LRTYCEASISNTTATRCPGPYPKREQDQYICRQDVRGNGCGFGKGKV VTCAKFSCSGKIKTENLVOLENTEYVUHNGDTHAQNHDGVTSPRSPEV EVKLPLDGYELTDCEPGRSLIDPNEMILMKMKCWTIYHKOMFLDLPLWTAGADTSEV HWNYKERMVTFKPHAKRQDVTWVGSAMHSALAGATEVGDGHNMFAGHLKCKV RMEKLRIKGMSYTMCSGRPSIDKEMAEOTQHGTIVKVEGAGAPCKPIERDVNE KVYGRVVISSTPLAENTNSVTNTEBLEPPGDSYIVIGVNSALAGATEVGDGHNMFAGHLKCKV STYRGAKRNAILGTADEGSVGLFTSGKAVHQHQSFSVYTMTGEVSWMRILIGF LVWIGTNSRNTSNAMTCIAVGGTILFLGFTVADMGCYVVSNSRELKCGS1FVVDN VHTWTEQYKFQFOPESPRLASALINAHKGVCVGRSTTRLENMWKOITNELN"
ORIGIN	
	Query Match 100.0%; Score 28; DB 14; Length 2552; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 0; Gaps 0; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	RESULT 49 AY152176S1
	Query Match 100.0%; Score 28; DB 14; Length 2552; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 0; Gaps 0; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	AY152176.1 GI:28171121
ORIGIN	
	Query Match 100.0%; Score 28; DB 14; Length 2552; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 0; Gaps 0; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	AY152176S1
	Query Match 100.0%; Score 28; DB 14; Length 2552; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 0; Gaps 0; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	AY152176.1 GI:28171121
RESULT 48	
AY152172S1	
LOCUS	AY152172S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION	Dengue virus type 4 D4_27_1992 polyprotein precursor, gene, partial cds.
ACCESSION VERSION	AY152172.1 GI:28171112
KEYWORDS	1 of 4
SOURCE	Dengue virus type 4 (DEN-4)
ORGANISM	Dengue virus type 4
FEATURES	Flavivirus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE	1 (bases 1 to 2552)
AUTHORS	Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
PUBMED	12832659
REFERENCE	1..2552
AUTHORS	Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vordam, V., Gubler, D.J. and McMillan, W.O.
TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES	Source
Source	1..2552
CDS	

THIS PAGE BLANK (USPTO)

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 11:21:31 ; Search time 203 Seconds
(without alignments)

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatatgtgaaacgcgagaaaaacgcgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %

Maximum Match 100 %

Listing First 50 Summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s;*

2: Geneseqn2000s;*

3: Geneseqn2001as;*

4: Geneseqn2001bs;*

5: Geneseqn2002as;*

6: Geneseqn2002bs;*

7: Geneseqn2003as;*

8: Geneseqn2003bs;*

9: Geneseqn2003bs;*

10: Geneseqn2003cs;*

11: Geneseqn2003ds;*

12: Geneseqn2004s;*

22 28 100.0 10649 10 AAD53910 Wild-type Dengue vi

23 28 100.0 10649 10 AAD53910 Dengue vi

24 28 100.0 10648 4 AAD14612 Wild-type Dengue vi

25 28 100.0 10648 4 AAD14612 Attenuate

26 28 100.0 10649 10 AAD53911 Recombina

27 28 100.0 10649 10 AAD53910 Wild-type Dengue vi

28 28 100.0 10649 10 AAD53910 Dengue vi

29 28 100.0 10649 10 AAD14607 Wild-type Dengue vi

30 28 100.0 10649 10 AAD14607 Attenuate

31 28 100.0 10649 10 AAD14607 Dengue vi

32 28 100.0 10649 10 AAD14607 Dengue vi

33 28 100.0 10649 10 AAD14607 Dengue vi

34 28 100.0 10649 10 AAD14607 Dengue vi

35 28 100.0 10649 10 AAD14607 Dengue vi

36 28 100.0 10649 10 AAD14607 Dengue vi

37 19.2 68.6 1083 3 AAC44997 Arabidops

38 19.2 68.6 1083 3 AAC44997 Arabidops

39 19.2 68.6 1083 3 AAC44997 Arabidops

40 19.2 68.6 1083 3 AAC44997 Arabidops

41 18.8 67.1 1008 3 AAC44997 Arabidops

42 18.6 66.4 3002 4 ABL29849 Drosophil

43 18.6 66.4 7264 4 ABL29849 Drosophil

44 18.4 65.7 449 3 AAA82355 N. mening

45 18.4 65.7 449 3 AAZ36161 DNA encod

46 18.4 65.7 1443 9 ABX16417 DNA encod

47 18.4 65.7 1647 12 ADP44354 1647bp se

48 18.4 65.7 4512 2 Aaq22767 JEV Nakay

49 18.4 65.7 10818 12 ADO07431 Japanese

50 18.4 65.7 10968 12 ADO07431 Japanese

51 18.4 65.7 10968 12 ADO07431 Japanese

ALIGNMENTS

RESULT 1

ABX15698

ID ABX15698 standard; DNA; 28 BP.

XX ABX15698;

AC ABX15698;

XX DT 31-MAR-2003 (first entry)

DE Dengue virus detection PCR primer #2.

XX XX

PCR; primer: ss; reverse transcriptase; RT-PCR; dengue fever; DF;

dengue haemorrhagic fever; virus; viral detection.

XX OS Dengue virus.

OS XX

US2002155435-A1.

XX PN

24-OCT-2002.

XX XX

28-FEB-2002; 2002US-0005944.

PP XX

01-MAR-2001; 2001US-0272535P.

PR XX

(WANG/) WANG W.

PA XX

New dengue virus-specific primers, useful for reverse transcriptase-

PT PT polymerase chain reaction assays, particularly for detecting or

quantitating dengue virus in a sample.

XX XX

Claim 28; Page 1; 6pp; English.

XX XX

New dengue virus reverse transcriptase (RT)

CC PT PCR primers which may be used to detect Dengue virus in a sample. Dengue

CC virus is a member of the Flavivirus family and causes diseases including

CC dengue fever (DF) and dengue haemorrhagic fever. The invention also

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	ABX15698	28	100.0	28	8	ABX15698	Dengue vi
2	ABX13740	28	100.0	2357	8	ABX13740	Dengue vi
3	ADG93319	28	100.0	2423	12	ADG93319	DEN1 (Pue
4	AAT47666	28	100.0	3381	2	AAT47666	Dengue vi
5	AAX25114	28	100.0	3381	2	AAX25114	Dengue vi
6	ADQ28715	28	100.0	3381	12	ADQ28715	Dengue vi
7	AAD14605	28	100.0	10616	10	AAD14605	Dengue vi
8	AAD14612	28	100.0	10648	4	AAD14612	Wild-type
9	AAD14613	28	100.0	10648	4	AAD14613	Attenuate
10	AAD53911	28	100.0	10649	10	AAD53911	Recombina
11	AAD53910	28	100.0	10649	10	AAD53910	Wild-type
12	AAD14607	28	100.0	10717	4	AAD14607	Dengue vi
13	AAG12787	28	100.0	10723	2	AAG12787	Dengue 2
14	AAT49303	28	100.0	10723	2	AAT49303	CDNA sequ
15	AAT49304	28	100.0	10723	2	AAT49304	CDNA enco
16	AAD14614	28	100.0	10723	4	AAD14614	Dengue vi
17	AAD14607	28	100.0	10723	4	AAD14607	Wild-type
18	AAD14608	28	100.0	10723	4	AAD14608	Dengue vi
19	AAD14608	28	100.0	10723	4	AAD14608	Attenuate
20	Adn98025	28	100.0	10724	12	ADN98025	Dengue vi
21	AAD14609	28	100.0	10756	4	AAD14609	Dengue vi

comprises a method for detecting and quantitating dengue virus. The dengue virus-specific primers of the invention are useful in reverse transcriptase-polymerase chain reaction assays. Particularly for detecting or quantitating dengue virus in a sample, the present sequence represents a dengue virus specific RT-PCR primer used in the method of the invention.

Sequence 28 BP; 11 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 28; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 AATATCCTGAAACGCCAGAGAAGAACCGCG 28
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AATATCCTGAAACGCCAGAGAAGAACCGCG 28
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
ABX13740
ID ABX13740 standard; DNA; 2357 BP.
XX AC
XX DT 28-FBB-2003 (first entry)
XX DE Dengue virus type 2 structural gene genome segment.
XX KW Pharmaceutical; ds; immune response; immunogenic; envelope; membrane; antigen; preM; dengue virus; Den; serotype; flaviviridae; antigen; mosquito; Aedes aegypti; acute undifferentiated fever; dengue haemorrhagic fever; DHF; dengue shock syndrome; DSS; immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine; structural gene; virucide.
XX OS Dengue virus.
XX PN US6455509-B1.
XX PD 24-SEP-2002.
XX PP 04-JUN-1997; 97US-00869423.
XX PR 04-JUN-1996; 96US-0017839P.
XX PA (USNA) US SEC OF NAVY.
XX PI Kochel TJ, Porter KR, Raviprakash K, Hoffman SL, Hayes CG,
WPI; 2003-066244/06.

RESULT 3
ADG33319
ID ADG33319 standard; DNA; 2423 BP.
XX AC
XX DT 11-MAR-2004 (first entry)
XX DE DEN1 (Puerto Rico/94) ME chimeric region DNA SeqID52.
XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
KW attenuating mutation; humoral response; cellular response; non-structural protein; dengue virus serotype; gene; ds; plasmid P2.
XX OS Dengue virus type 1.
XX PN WO2003092592-A2.
XX PD 13-NOV-2003.
XX PF 25-APR-2003; 2003WO-US013279.
XX PR 03-MAY-2002; 2002US-0377860P.
XX PR 23-DEC-2002; 2002US-0436500P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
PI Hanley K;
XX DR WPI; 2004-022612/02.
XX DR P-PSDB; ADG93320.

Query Match 100.0%; Score 28; DB 8; Length 2357;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCCAGAGAAGAACCGCG 28
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 AATATGCTGAAACGCCAGAGAAGAACCGCG 87

RESULT 3
ADG33319
ID ADG33319 standard; DNA; 2423 BP.
XX AC
XX DT 11-MAR-2004 (first entry)
XX DE DEN1 (Puerto Rico/94) ME chimeric region DNA SeqID52.
XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
KW attenuating mutation; humoral response; cellular response; non-structural protein; dengue virus serotype; gene; ds; plasmid P2.
XX OS Dengue virus type 1.
XX PN WO2003092592-A2.
XX PD 13-NOV-2003.
XX PF 25-APR-2003; 2003WO-US013279.
XX PR 03-MAY-2002; 2002US-0377860P.
XX PR 23-DEC-2002; 2002US-0436500P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
PI Hanley K;
XX DR WPI; 2004-022612/02.
XX DR P-PSDB; ADG93320.

Disclosure; SEQ ID NO 52; 181pp; English.

This invention relates to a novel immunogenic composition being tetravalent and containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4. The invention may be useful for the development of compounds with a virucide or immunostimulant activity or as a vaccine. The tetravalent vaccine is useful in the prevention of disease in humans caused by dengue virus. Unlike previous tetravalent vaccine, the new tetravalent vaccine is unique since they contain a common shared attenuating mutation which eliminates the possibility of generating a virulent wild type virus in a subject to be vaccinated since each component of the vaccine possesses the same delta30 attenuating deletion mutation. The vaccine also is able to induce humoral and cellular responses against all of the (non-structural proteins present in each dengue virus serotype. The present sequence is that of the DEN1 MB chimeric region DNA which is related to the invention.

XX Sequence 2423 BP; 747 A; 513 C; 636 G; 527 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 28; DB 12; Length 2423;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; MisMatches 0; Other;

Qy 1 AATATGCTGAAACGGAGAAACCCG 28
 Db 138 AATATGCTGAAACGGAGAAACCCG 165

RESULT 4
 AAT47666
 ID AAT47666 standard; cDNA; 3381 BP.
 XX AC AAT47666;
 XX DT 17-OCT-2003 (revised)
 DT 19-MAY-1997 (first entry)
 XX DE Dengue virus serotype 2 PR159/S1 mutant sequence.
 KW DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.
 OS Dengue virus; serotype 2.
 XX Key Location/Qualifiers
 PH Mutation 1216..1218
 FT /note= "codon GAG (Glu) at position 1216-1218 of PR159/S1
 is GAA (Glu) in wild-type PR159"
 FT /note= "codon GTT (Val) at position 1258-1260 of PR159/S1
 is GTG (Val) in wild-type PR159"
 FT /note= "codon GTT (Val) at position 1762-1764 of PR159/S1
 is ATT (Tle) in wild-type PR159"
 FT /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1
 is ACT (Ser) in wild-type PR159"
 XX WO9637221-A1.
 XX PD 28-NOV-1996.
 XX PF 24-MAY-1996; 96WO-US007627.
 XX PA (HAWAII BIOTECHNOLOGY GROUP INC.
 PI Ivy JM, Nakano E, Clements D;
 PR 24-MAY-1995; 95US-00448734.
 PR 07-JUN-1995; 95US-00488807.
 PR 10-JUL-1995; 95US-00500469.
 XX DR WPI; 1997-020938/02.
 DR P-PSDB; AAW09403.

PS Sub:unit vaccine against flavivirus infection - contg; recombinant
 PT envelope protein in secretable form, used for immunising against
 PT flavivirus infection.
 XX Example 1; Fig 3A-D; 121pp; English.

CC A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1
 CC shows 4 differences from the wild-type PR159. This results in a
 CC conservative mutation in domain B of S1 that may be involved in the
 CC attenuation of this small-plaque, temp-sensitive variant. The cDNA
 CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of

XX the virus. The clone can be used to express recombinant secreted
 CC polypeptides, comprising portions of the envelope protein (esp. domain B,
 CC Gly996-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47667 and
 CC AAT47703-04), and Drosophila, for use in subunit vaccines against viral
 CC infection. (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
 XX Query Match 100.0%; Score 28; DB 2; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; MisMatches 0; Other;

Qy 1 AATATGCTGAAACGGAGAAACCCG 28
 Db 40 AATATGCTGAAACGGAGAAACCCG 67

RESULT 5
 AAX25114
 ID AAX25114 standard; cDNA; 3381 BP.
 XX AC AAX25114;
 XX DE Dengue virus serotype 2 PR159/S1 viral capsid, pprM, E, NS1 cDNA.
 KW Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.
 OS Dengue virus; serotype 2.
 XX PN WO9306068-A2.
 XX PD 11-FEB-1999.
 XX PR 27-JUL-1998; 98WO-US015447.
 XX PR 31-JUL-1997; 97US-00904227.
 XX PA (HAWAII BIOTECHNOLOGY GROUP INC.
 PI Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KE;
 XX WPI; 1999-153454/13.
 DR P-PSDB; AAY05322.
 XX PT Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric
 PT 80% protein, useful for protecting against flavivirus, especially dengue
 PT virus infections.
 XX PS Example 1; Fig 3A-D; 60pp; English.
 XX This cDNA sequence encodes the capsid, pprM, envelope (E) and NS1 Proteins
 CC (see AAY05322) of serotype 2 dengue virus DEN-2 strain PR159/S1. This
 CC strain served as the source for DEN-2 genes used in the invention. A dimeric
 CC vaccine for protecting against flavivirus infection comprises a dimeric
 CC 80% E protein that has been secreted as recombinant protein from a
 CC eukaryotic cell. 80% E indicates a C-terminally truncated Flavivirus E.
 CC The dimeric truncated E is formed: (1) by directly linking 2 tandem
 CC copies of 80% E via a flexible tether; (2) via the formation of a leucine
 CC zipper domain through the homodimeric association of 2 leucine zipper
 CC helices each fused to the C-terminus of an 80% E molecule; or (3) via the
 CC formation of a non-covalently associated four-helix bundle domain formed
 CC upon association of two helix-turn-helix moieties attached to the C-
 CC terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
 CC efficiently secreted by recombinant cells, are easier to purify than
 CC intracellular proteins, and generate a high titer neutralising antibody
 CC response. The method is generally applicable to flaviviruses, in
 CC particular dengue viruses such as DEN-2, where 80% E comprises amino
 CC acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
 CC infection. (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 2; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTAAACGCCAGAGAACCCCG 28
 Db 40 AATATGCTAAACGCCAGAGAACCCCG 67

RESULT 6
 ID ADQ28715 standard; DNA; 3381 BP.

XX AC ADQ28715;
 XX DT 26-AUG-2004 (first entry)
 DE Dengue virus viral capsid, prM, E and NS1 genes.
 XX KW viricide; vaccine; Flavivirus; dimeric 80%E; Drosophila Schneider cell;
 KW immunogenic composition; multivalent immunodiagnostic; dengue virus;
 KW viral capsid; prM gene; E gene; NS1 gene; ds.
 XX OS Dengue virus.

XX FH Key
 FT CDS 1. .3381
 FT /*tag= a
 FT /product= "Dengue virus viral capsid, prM, E and NS1."
 FT /product= "polyprotein"

XX PN US6749857-B1.
 XX PD 15-JUN-2004.
 XX PF 18-AUG-1999; 99US-00376463.
 XX PR 31-JUL-1997; 97US-00904227.
 XX PA (HAWA) HAWAII BIOTECHNOLOGY GROUP INC.
 XX Peters ID, Collier BG, McDonell M, Ivy JM, Harada K;
 XX WPI; 2004-438725/41.
 DR PSDB; ADQ28716.

XX New vaccines for preventing or diagnosing infections caused by dengue virus comprises a therapeutic amount of a dimeric 80%E protein secreted from Drosophila Schneider cells.

PS Example 1; SEQ ID NO 2; 47pp; English.

XX The invention describes a vaccine that generates a protective, neutralising antibody response to a Flavivirus in a murine host. The vaccine comprises a therapeutic amount of a dimeric 80%E, the dimeric 80%E having been secreted as a recombinantly produced protein from Drosophila Schneider cells, and where 80%E represents the N-terminal 80% portion of the protein from residues 1-395. Also described are: an immunogenic polypeptide comprising the dimeric 80%E cited above; an antibody response to a Flavivirus in a murine host, comprising the above immunogenic polypeptide and a physiochemical carrier, a multivalent immunodiagnostic for the detection of Flavivirus, comprising at least 2 of the above immunogenic polypeptides of at least 2 flaviviral serotypes; and an immunoassay kit for the detection of Flavivirus in a test subject, comprising the above immunogenic or multivalent immunodiagnostic polypeptide, a suitable support phase coated with dimeric 80%E, and labelled antibodies immunoreactive to antibodies from the test subject. The composition is useful for preventing or diagnosing infections caused by dengue virus. This sequence encodes Dengue virus gene viral capsid, prM, E and NS1 genes for Dengue virus strain PR159/S1 used as the source

CC CC of DEN-2 genes for the invention.

XX XX Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 28; DB 12; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTAAACGCCAGAGAACCCCG 28
 Db 40 AATATGCTAAACGCCAGAGAACCCCG 67

RESULT 7
 ID AAD3912 standard; DNA; 10616 BP.

XX AC AAD3912;
 XX DT 28-MAY-2003 (first entry)
 DE Dengue virus type 2 strain rDEN2/4delta30 DNA.
 XX KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
 XX OS Dengue virus.

XX FH Key
 FT CDS 97..10263
 FT /*tag= a
 FT /product= "DEN4 strain rDEN2/4delta30 protein"
 FT mat_peptide 97..438
 FT /*tag= c
 FT /product= "Anchored capsid protein"
 FT mat_peptide 97..396
 FT /*tag= b
 FT /product= "Virion capsid protein"
 FT mat_peptide 439..936
 FT /*tag= d
 FT /product= "Membrane precursor protein"
 FT mat_peptide 712..936
 FT /*tag= e
 FT /product= "Membrane protein"
 FT mat_peptide 937..2421
 FT /*tag= f
 FT /product= "Envelope protein"
 FT mat_peptide 2422..3477
 FT /*tag= g
 FT /product= "NS1 protein"
 FT mat_peptide 3478..4131
 FT /*tag= h
 FT /product= "NS2A protein"
 FT mat_peptide 4132..4521
 FT /*tag= i
 FT /product= "NS2B protein"
 FT mat_peptide 4522..6375
 FT /*tag= j
 FT /product= "NS3 protein"
 FT mat_peptide 6376..6756
 FT /*tag= k
 FT /product= "NS4A protein"
 FT mat_peptide 6757..6825
 FT /*tag= l
 FT /product= "NS4B protein"
 FT mat_peptide 6826..7560
 FT /*tag= m
 FT /product= "NS4B protein"
 FT mat_peptide 7561..10260
 FT /*tag= n
 FT /product= "NS5 protein"
 PN WO200295075-A1.

FT	mutation	replace(7162, T)	Location/Qualifiers
FT	mutation	/*tag= g	/tag= a
FT	mutation	replace(7546, C)	/product= "DEN4 strain rDEN4 protein"
FT	mutation	/*tag= h	103..10649
FT	mutation	replace(7623, G)	/*tag= b
FT	mutation	/*tag= i	/*tag= c
XX	WO200160847-A2.		/product= "Anchored capsid protein"
XX	23-AUG-2001.		
XX	16-FEB-2001; 2001WO-WS005142.		
XX	16-FEB-2000; 2000US-0182829P.		
PR	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
XX	Kirnay RH, Kirnay CYH, Butrapet S, Gubler DJ, Bhamarapravati N;		
PI	WPI: 2001-497162/54.		
DR	P-PSDB; AAE07932.		
XX	Example 4; Page 397-413; 470pp; English.		
PS	Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.		
XX	The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuated-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1 to DEN-4), are mosquito-borne Flavivirus pathogens. The flavivirus genome contains 5, non-coding region followed by a capsid protein (pM) encoding region, premembrane/membrane protein (prM) encoding region, an envelope protein (E) encoding region, followed by the region encoding non-structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3' non-coding region. DEN-4 virus passed in primary dog kidney (PDK) cells 48 times is designated as DEN-4 PDK-48 virus		
XX	Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;		
SQ	Query Match 100.0%; Score 28; DB 4; Length 10648;		
	Best Local Similarity 100.0%; Pred. No. 0.013;		
	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 ATATGCTGAAACGGAGAGAAACCGCG 28		
Ddb	138 ATATGCTGAAACGGAGAGAAACCGCG 165		
RESULT 10			
AAD33911	Recombinant dengue virus type 4 strain rDEN4 DNA.		
ID	AAD53911 standard; DNA; 10649 BP.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
AC	AAD53911;		
XX	28-MAY-2003 (first entry)		
PS	RESULT 10		
DT	AAD33911		
XX	Recombinant dengue virus type 4 strain rDEN4 DNA.		
DE	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		
DE	Dengue virus.		
XX	AAD53911;		
AC	28-MAY-2003 (first entry)		
XX	RESULT 10		
PS	AAD33911		
DT	Recombinant dengue virus type 4 strain rDEN4 DNA.		
XX	Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.		

CC useful for fine tuning the attenuation and growth characteristics of
 CC dengue virus vaccines for the prevention and/or treatment of dengue virus
 XX infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA
 SQ Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 10; Length 10649;
 Best Local Similarity 100.0%; Pred. No. 0.013; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES .
 PA (BLAN) / BLANEY J E.
 PA Whitehead SS, Murphy BR, Hanley KA;
 PI Whitehead SS, Murphy BR, Hanley KA;
 XX WPI; 2003-120809/11.
 DR DR P-PSDB; AAE35312.
 XX P-PSDB; AAE35312.

RESULT 11

AAD53910 standard; DNA; 10649 BP.
 ID AAD53910
 XX
 AC AAD53910;
 XX DT 28-MAY-2003 (first entry)
 DE Dengue virus type 4 strain 2A DNA.
 XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
 KW XX
 OS Dengue virus.
 FT Key
 FH CDS
 FT /product= "DEN4 strain 2A protein"
 FT /tag= a
 FT /tag= c
 FT /product= "Anchored capsid protein"
 FT /tag= b
 FT /product= "Virion capsid protein"
 FT /tag= d
 FT /product= "Membrane precursor protein"
 FT /tag= e
 FT /product= "Membrane protein"
 FT /tag= f
 FT /product= "Envelope protein"
 FT /tag= g
 FT /product= "NS1 protein"
 FT /tag= h
 FT /product= "NS2A protein"
 FT /tag= i
 FT /product= "NS2B protein"
 FT /tag= j
 FT /product= "NS3 protein"
 FT /tag= k
 FT /product= "NS4A protein"
 FT /tag= l
 FT /product= "2K protein"
 FT /tag= m
 FT /product= "NS4B protein"
 FT /tag= n
 FT /product= "NS5 protein"
 XX

XX WO200295075-A1.
 XX PD 28-NOV-2002.
 XX PR 22-MAY-2002; 2002WO-US016308.
 XX PR 22-MAY-2001; 2001US-0293049P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES .
 PA (BLAN) / BLANEY J E.
 PA Whitehead SS, Murphy BR, Hanley KA;
 PI Whitehead SS, Murphy BR, Hanley KA;
 XX WPI; 2003-120809/11.
 DR DR P-PSDB; AAE35312.

XX New mutated flavivirus, useful for fine tuning the attenuation and growth
 PT characteristics of dengue virus vaccines for the prevention and/or
 PT treatment of dengue virus infection.
 XX Disclosure; Page 123-126; 246PP; English.

XX PS
 XX CC The present invention relates to novel mutated flaviviruses comprising a
 CC phenotype in which the viral genome is modified by introduction of a
 CC mutation, singly or in combination, taken from mutations from recombinant
 CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
 CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
 CC dengue type 4 virus. The methods and compositions of the invention are
 CC useful for fine tuning the attenuation and growth characteristics of
 CC dengue virus vaccines for the prevention and/or treatment of dengue virus
 CC infection. The present sequence is Dengue virus type 4 strain 2A DNA
 XX Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 28; DB 10; Length 10649;
 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;

XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAAACCGCG 28
 Db 138 AATATGCTGAAACGGAGAGAACCGCG 165

RESULT 12

AADI4605

ID AADI4605 Standard; cDNA; 10717 BP.
 XX
 AC AADI4605;
 XX DT 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX DE Dengue virus (DEN)-2/3-VP1 chimeric cDNA.
 XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
 XX OS Dengue virus; type II.
 OS Dengue virus; type III.
 OS Chimeric.
 XX FH Key
 FT CDS
 XX Location/Qualifiers
 97. 10366
 /*tag= a
 /product= "DEN-2/3-VP1 fusion protein"

XX FT
 XX FT
 XX PR
 XX WO200160847-A2.
 XX PD 23-AUG-2001.

XX FT
 XX PR 16-FEB-2001; 2001WO-US005142.
 XX PR 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES .
 XX PA Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarabratavi N;
 XX PI WPI; 2001-497162/54 .
 XX DR P-PSDB; AAE07984 .
 XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccination against a range of dengue viruses.
 XX PS Example 2; Page 203-219; 470pp; English.
 XX CC The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes dengue virus (DEN-2/3-VP1) fusion protein related to the
 CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 CC comprising a valine at the non-structural protein (NS2) -250 and the
 CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
 CC type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
 SQ Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;
 SQ Score 28; DB 4; Length 1017;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 AATATCCTGAAACGGAGAGAAACCCG 28
 Db 136 AATATGCTGAAACGGAGAGAAACCGCG 163
 YY RESULT 13
 ID AAQ12787 Standard; RNA; 10723 BP.
 AC AAQ12787;
 XX DT 25-MAR-2003 (revised)
 DT 21-NOV-1991 (first entry)
 XX DE Dengue 2 virus genome.
 KW dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
 OS Dengue virus.
 XX Key Location/Qualifiers
 FH 97. .10272
 FT / *tag= a
 mat_peptide 712. .936
 FT / *tag= b
 FT /product= "M protein"
 mat_peptide 937. .2421
 FT / *tag= c
 FT /product= "E protein"
 mat_peptide 2422. .3477
 FT / *tag= d
 FT /product= "NS1"
 mat_peptide 3478. .4131
 FT / *tag= e
 FT /product= "NS2A"
 mat_peptide 4132. .4518
 FT
 FT /*tag= f
 /product= "NS2B"
 4519. .6375
 FT mat_peptide
 FT /*tag= g
 /product= "NS3"
 6376. .6825
 FT mat_peptide
 FT /*tag= h
 /product= "NS4a"
 6826. .7569
 FT mat_peptide
 FT /*tag= i
 /product= "NS4B"
 7570. .10269
 FT mat_peptide
 FT /*tag= j
 /product= "NS5"
 XX FR2654113-A.
 PN 10-MAY-1991.
 PD 09-NOV-1989;
 XX 89FR-00914724.
 PR 09-NOV-1989;
 XX (INSP) INST PASTEUR.
 PA Vincent D;
 XX DR WPI; 1991-2250102/31.
 DR P-PDB; AARI13166.
 XX Detection and identification of Flaviviridae in biological sample - by
 PT amplifying consensus sequence then hybridisation opt. followed by typing,
 PR e.g. sequencing amplified prod.
 XX Disclosure: Fig 3; 24pp; French.
 PS
 XX CC The dengue 2 virus is an example of a member of the Flaviviridae which
 CC can be identified using the probe pair of the invention. A species-
 CC specific sequence can be amplified using the claimed oligonucleotides as
 CC primers in a PCR reaction (see AAQ12787 and AAQ12789). Other viruses
 CC which can be identified include Japanese encephalitis virus and yellow
 CC fever virus. (Updated on 25-MAR-2003 to correct PR field.)
 XX SQ Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;
 PS Query Match 100.0%; Score 28; DB 2; Length 10723;
 Best Local Similarity 89.3%; Pred. No. 0.013;
 Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 YY Qy 1 AATATGCTGAAACGGAGAGAAACCCG 28
 Db 136 AATATGCTGAAACGGAGAGAAACCGCG 163
 YY RESULT 14
 ID AAT49303 standard; cdNA; 10723 BP.
 AC AAT49303;
 XX DT 27-AUG-2003 (revised)
 DT 11-SEP-1997 (first entry)
 XX DB CDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
 XX KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS5B; NS5; PDK-53; quadrivalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 KW DHF; DSS; 86.
 XX OS Dengue virus type 2 (strain 16681).
 FT

XX Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;

SQ Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATAAGCTTAAACGCGAGAACGGCG 28
Db 136 AATAAGCTTAAACGCGAGAACGGCG 163

RESULT 16
ID AAD14614 Standard; cDNA; 10723 BP.

XX AAD14614;
AC AAD14614;
XX DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX DE Dengue virus (DEN) -2/1-VP1 chimeric cDNA.
XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent; immunogenic; viral disease; pharmaceutical; chimeric; ss.

OS Dengue virus; type I.
OS Dengue virus; type II.
OS Chimeric.

FH Key
FT CDS Location/Qualifiers
FT FT 97. 10272
FT FT /*tag= a
/product= "DEN-2/1-VP1 fusion protein"
FT FT /*tag= a
/product= "DEN-2/1-VP1 fusion protein"

XX PN WO20010847-A2.
XX PD 23-AUG-2001.
XX PR 16-FEB-2001; 2001WO-US005142.

XX PF 16-FEB-2001; 2001WO-US005142.
XX PR 16-FEB-2000; 2000US-0182829P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Kinney RM, Butrapet S, Gubler DL, Bhamarapravati N;
XX DR WPI; 2001-497162/54.
XX PT P-PSDB; AAE07986.

XX PI Kinney RM, Kirney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX DR WPI; 2001-497162/54.
XX PT P-PSDB; AAE07993.

XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccination against a range of dengue viruses.

XX PS Example 5; Page 422-438; 470pp; English.

CC The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flaviviruses chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes wild-type, virulent dengue-2 (DEN-2), 1681 virus protein used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1 to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome contains 5' non-coding region followed by a capsid protein (C) encoding region, premembrane/membrane protein (prM) encoding region, an envelope protein (E) encoding region, followed by the region encoding non-structural proteins (NS1-NS2-NS3-NS4A-NS4B-NS5) and finally a 3'-non-coding region. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGCGAGAACGGCG 28
DB 136 AATATGCTGAAACCGCGAGAACGGCG 163

RESULT 17
ID AAD14607 Standard; cDNA; 10723 BP.

XX AC AAD14607;
XX DT 11-JEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX DB Wild-type, virulent DEN-2 16681 cDNA.

XX KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; avirulent; immunogenic; viral disease; pharmaceutical; ss.

XX OS Dengue virus; type II.

XX FH Key
FT CDS Location/Qualifiers
FT FT 97. 10272
FT FT /*tag= a
/product= "DEN-2 16681 protein"

XX PN WO20010847-A2.
XX PD 23-AUG-2001.
XX PR 16-FEB-2001; 2001WO-US005142.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Kinney RM, Butrapet S, Gubler DL, Bhamarapravati N;
XX DR WPI; 2001-497162/54.
XX PT P-PSDB; AAE07986.

XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccination against a range of dengue viruses.

XX PS Example 3; Page 252-268; 470pp; English.

CC The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flaviviruses chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes wild-type, virulent dengue-2 (DEN-2), 1681 virus protein used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1 to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome contains 5' non-coding region followed by a capsid protein (C) encoding region, premembrane/membrane protein (prM) encoding region, an envelope protein (E) encoding region, followed by the region encoding non-structural proteins (NS1-NS2-NS3-NS4A-NS4B-NS5) and finally a 3'-non-coding region. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 4; Length 10723;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 1 AATATGCTGAACGCCAGAGAAACCCG 28
 Db 136 AATATGCTGAACGCCAGAGAAACCCG 163

RESULT 18
 AAD14608
 ID AAD14608 standard; cDNA; 10723 BP.
 XX
 AC AAD14608;
 XX DT 11-SEP-2003 (revised)
 DT . 01-NOV-2001 (first entry)
 XX DE Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.
 XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; mutant;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
 XX KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
 XX KW ss.
 XX Dengue virus; type II.
 OS Synthetic.
 OS Dengue virus; type IV.
 OS Chimeric.
 XX FH Key Location/Qualifiers
 FH FT 97. 10272
 FT FT /*tag= a
 FT FT /product= "DEN-2/4-VPI fusion protein"
 FT FT XX WO200160847-A2.
 XX PD 23-AUG-2001.
 XX PF 16-FEB-2001; 2001WO-US005142.
 XX PR 16-FEB-2000; 2000US-0182829P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
 XX DR WPI; 2001-497162/54.
 DR P-PSDB; AAB07955.
 XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX PS Example 3; Page 227-243; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes dengue virus (DEN)-2/4-VPI fusion protein related to the
 CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 CC comprising a valine at the non-structural protein (NS1) -250 and the
 CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
 CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 1 AATATGCTGAACGCCAGAGAAACCCG 28
 Db 136 AATATGCTGAACGCCAGAGAAACCCG 163

RESULT 19
 AAD14608
 ID AAD14608 standard; cDNA; 10723 BP.
 XX AC AAD14608;
 XX DT 01-NOV-2001 (first entry)
 XX DB Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.
 XX KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; mutant;
 KW immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.
 XX Dengue virus; type II.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FH FT mutation
 FT FT replace(57, C)
 FT FT /*tag= b
 FT FT CDS
 FT FT /*tag= a
 FT FT /product= "DEN-2 PDK-53 protein variant"
 FT FT replace(524, A)
 FT FT /*tag= C
 FT FT replace(2055, C)
 FT FT /*tag= b
 FT FT replace(2579, G)
 FT FT /*tag= a
 FT FT replace(4018, C)
 FT FT /*tag= f
 FT FT replace(25270, A)
 FT FT /*tag= d
 FT FT replace(5547, T)
 FT FT /*tag= e
 FT FT replace(6599, G)
 FT FT /*tag= i
 FT FT replace(8571, C)
 FT FT /*tag= j
 XX PN WO200160847-A2.
 XX PD 23-AUG-2001.
 XX PR 16-FEB-2001; 2001WO-US005142.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
 XX DR WPI; 2001-497162/54.
 DR P-PSDB; AAB07955.
 XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX PS Example 3; Page 227-243; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes dengue virus (DEN)-2/4-VPI fusion protein related to the
 CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 CC comprising a valine at the non-structural protein (NS1) -250 and the
 CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
 CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 1 AATATGCTGAACGCCAGAGAAACCCG 28
 Db 136 AATATGCTGAACGCCAGAGAAACCCG 163

RESULT 19
 AAD14608
 ID AAD14608 standard; cDNA; 10723 BP.
 XX AC AAD14608;
 XX DT 01-NOV-2001 (first entry)
 XX DB Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.
 XX KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; mutant;
 KW immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.
 XX Dengue virus; type II.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FH FT mutation
 FT FT replace(57, C)
 FT FT /*tag= b
 FT FT CDS
 FT FT /*tag= a
 FT FT /product= "DEN-2 PDK-53 protein variant"
 FT FT replace(524, A)
 FT FT /*tag= C
 FT FT replace(2055, C)
 FT FT /*tag= b
 FT FT replace(2579, G)
 FT FT /*tag= a
 FT FT replace(4018, C)
 FT FT /*tag= f
 FT FT replace(25270, A)
 FT FT /*tag= d
 FT FT replace(5547, T)
 FT FT /*tag= e
 FT FT replace(6599, G)
 FT FT /*tag= i
 FT FT replace(8571, C)
 FT FT /*tag= j
 XX PN WO200160847-A2.
 XX PD 23-AUG-2001.
 XX PR 16-FEB-2001; 2001WO-US005142.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
 XX DR WPI; 2001-497162/54.
 DR P-PSDB; AAB07955.
 XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX PS Example 3; Page 227-243; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes dengue virus (DEN)-2/4-VPI fusion protein related to the
 CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 CC comprising a valine at the non-structural protein (NS1) -250 and the
 CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
 CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;

C structural genes of the virus are used as a backbone into which the C structural protein genes of a second Flavivirus strain are inserted. C These chimeric viruses elicit pronounced immunogenicity but lack the C accompanying clinical symptoms of viral disease. Attenuated chimeric C flaviviruses are combined in a pharmaceutical composition to confer C simultaneous immunity against several strains of pathogenic flaviviruses C such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic C flavivirus chimeras are also used as immunogens or multivalent vaccines C to confer simultaneous protection against infections. The present cDNA C sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant C used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1 to C DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome C contains 5' non-coding region followed by a capsid protein (C) encoding C region, premembrane membrane protein (prM) encoding region, an envelope C protein (E) encoding region, followed by the region encoding non- C structural proteins (NS1-NS2a-NS2a-NS3-NS4a-NS4b-NS5) and finally a 3' C non-coding region.

A	Q	Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;
	Query Match	100.0%; Score 28; DB 4; Length 10723;
	Best Local Similarity	100.0%; Pred. No. 0.013;
	Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps
1	Y	AATATGCTGAAACGCCGAGAGAAACGGCG 28
136	b	AATATGCTGAAACGCCGAGAGAAACGGCG 163

RESULT 20
DN98025 D ADN98025 standard; DNA; 10724 BP.
X C ADN98025;
Y C

Dengue Virus isolate New Guinea complete genome sequence.
X X T T 29-JUL-2004 (first entry)

X Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.

WO2004040263-A2
Dengue virus.

D 13 - MAY - 2004.

31-OCT-2003; 2003WO-US034823;

31-OCT-2002; 2002US-0422755P.

06-004-2003; 20030604/0035.

תְּמִימָנָה / מִשְׁמָרָה וְמִשְׁמָרָה

XII
מִנְחָה
לְפָרָשָׁת
בְּנֵי
יִשְׂרָאֵל

卷之三

new diagnostic tool comparing sera from *WNV* and *DENV* patients to those from *SLEV* and *JEV* patients.

The invention relates to a diagnostic kit comprising at least one isolated and purified polypeptide comprising a West Nile Virus (WNV) envelope (E) protein or its immunogenic fragment having a native conformation or non-denatured structure and that is reactive with antibodies against WNV and cross-reactive with antibodies against a flavivirus. The diagnostic kit is useful in diagnosing flavivirus infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to Disclosure; Fig 40; 212pp; English.

CC the complete nucleotide sequence of the DENV isolate New Guinea.
 XX Sequence 10724 BP; 3542 A; 2212 C; 2725 G; 2245 T; 0 U; 0 Other;
 SQ Query Match 100 %; Score 28; DB 12; Length 10724;
 Best Local Similarity 100 %; Pred. NO. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; G

Qy	1 AATATGTGAAACCGAGAGAACCGCG 28
Db	136 AATATGTGAAACCGAGAGAACCGC 163

RESULT 21
 AAD14609
 ID AAD14609 standard; cDNA; 10756 BP.
 XX
 AC AAD14609;
 XX
 DT 11-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX
 DE Dengue virus (DEN) -2/WN-PP1 chimeric cDNA.
 XX
 KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric;
 KW ss.

	Location/Qualifiers	
	Key	
AA		
OS	Dengue virus; type II.	
OS	West Nile virus.	
OS	Chimeric.	
XX		
FH		
CDS		
		/*tag= a
		/product= "DBN-2/WN-PP1 fusion protein"

PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX PF 16-FEB-2001; 2001WO-US005142.
XX PR 16-FEB-2000; 2000US-0182829P.
XX

XX	Kinney RM,	Kinney CYH,	Butrapet S,	Gubler DL,	Bhamarapravati N;
PI					
XX					
DR	WPI; 2001-497162/54.				
DR	P-PSDB; AAE07988.				
XX					
PT					Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT					vaccinating against a range of dengue viruses.
PT					

PS Example 6; Page 300-316; 470pp; English.

The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity, but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present CDNA sequence encodes dengue virus (DEN)-2/WN-PPI fusion protein related to the invention. This fusion protein contains DEN-2 1661 backbone and the membrane protein (prM) and an envelope protein (E) from West Nile NY99. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-mile NY99.

CC SEP-2003 to standardise OS field)
 XX Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 28; DB 4; Length 10756;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAAAACCGCG 28
 Db 136 AATATGCTGAAACGGAGAAAACCGCG 163

RESULT 22
 ADG9313 standard; DNA; 15159 BP.
 XX ID ADG9313 standard; DNA; 15159 BP.
 AC ADG9313;
 XX DT 11-MAR-2004 (first entry)
 DE DENV (Tonga/74) cDNA plasmid P2.
 KW immunogenic composition; dengue type 1; dengue type 3;
 KW dengue virus; dengue type 4; viricide; immunostimulant; vaccine; tetravalent vaccine;
 KW dengue virus; delta10; attenuating mutation; humoral response;
 KW cellular response; non-structural protein; structural protein;
 KW dengue virus serotype; gene; ds; plasmid P2.
 OS Dengue virus type 2.
 XX PN WO2003092592-A2.
 PD 13-NOV-2003.
 XX PF 25-APR-2003; 2003WO-US013279.
 PR 03-MAY-2002; 2002US-0377860P.
 PR 23-DEC-2002; 2002US-0436500P.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
 XX PI Hanley K;
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PT New tetravalent vaccine containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4, useful for preventing disease in humans caused by dengue virus, or for inducing immune response.
 XX Disclosure: SEQ ID NO 50; 181PP; English.
 PS This invention relates to a novel immunogenic composition being
 CC tetralvalent and containing a common nucleotide deletion in the 3'
 CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
 CC useful for the development of compounds with a virucide or
 CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
 CC useful in the prevention of disease in humans caused by dengue virus.
 CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
 CC unique since they contain common shared attenuating mutation which
 CC eliminates the possibility of generating a virulent wild type virus in a
 CC subject to be vaccinated since each component of the vaccine possesses
 CC the same delta10 attenuating deletion mutation. The vaccine also is able
 CC to induce humoral and cellular responses against all of the (non-
 CC structural proteins present in each dengue virus serotype. The present
 CC sequence is that of the DEN1 cDNA plasmid P2 which is related to the
 CC invention.
 XX Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other;
 SQ Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 12; Length 15159;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAAAACCGCG 28
 Db 136 AATATGCTGAAACGGAGAAAACCGCG 163

RESULT 23
 ADG9317 standard; DNA; 2426 BP.
 XX ID ADG9317 standard; DNA; 2426 BP.
 AC ADG9317;
 XX DT 11-MAR-2004 (first entry)
 XX DE DEN1 (Puerto Rico/94) CME chimeric region DNA SeqID50.
 XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
 KW dengue type 4; viricide; immunostimulant; vaccine; tetravalent vaccine;
 KW dengue virus; delta10; attenuating mutation; humoral response;
 KW cellular response; non-structural protein; structural protein;
 KW dengue virus serotype; gene; ds; plasmid P2.
 OS Dengue virus type 1.
 XX PN WO2003092592-A2.
 PD 13-NOV-2003.
 XX PF 25-APR-2003; 2003WO-US013279.
 PR 03-MAY-2002; 2002US-0377860P.
 PR 23-DEC-2002; 2002US-0436500P.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
 XX PI Hanley K;
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PT New tetravalent vaccine containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4, useful for preventing disease in humans caused by dengue virus, or for inducing immune response.
 XX Disclosure: SEQ ID NO 50; 181PP; English.
 PS This invention relates to a novel immunogenic composition being
 CC tetralvalent and containing a common nucleotide deletion in the 3'
 CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
 CC useful for the development of compounds with a virucide or
 CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
 CC useful in the prevention of disease in humans caused by dengue virus.
 CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
 CC unique since they contain common shared attenuating mutation which
 CC eliminates the possibility of generating a virulent wild type virus in a
 CC subject to be vaccinated since each component of the vaccine possesses
 CC the same delta10 attenuating deletion mutation. The vaccine also is able
 CC to induce humoral and cellular responses against all of the (non-
 CC structural proteins present in each dengue virus serotype. The present
 CC sequence is that of the DEN1 cDNA plasmid P2 which is related to the
 CC invention.
 XX Sequence 2426 BP; 754 A; 509 C; 632 G; 531 T; 0 U; 0 Other;
 SQ Query Match 94.3%; Score 26.4; DB 12; Length 2426;
 Best Local Similarity 96.4%; Pred. No. 0.059;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGGAGAGAACCCCG 28
 Db 141 AATATGCTGAAACGGAGAGAACCCCG 168

RESULT 24
 AAQ51476 AAQ51476 standard; DNA; 10718 BP.

XX AC AAQ51476;
 XX DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 16-MAY-1994 (first entry)
 XX DE DENV-S275/90 (ECACC V92042111).
 KW Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock syndrome;
 XX DSS; DEN1 polypeptides; ss.
 OS Dengue virus type 2.

XX FH Key Location/Qualifiers
 CDS 81. .10271
 FT misc_RNA /*tag= a
 FT misc_RNA 81. .422
 FT misc_RNA /*tag= b
 FT misc_RNA 123. .422
 FT misc_RNA /*tag= c
 FT misc_RNA 423. .695
 FT misc_RNA /*tag= d
 FT misc_RNA 696. .920
 FT misc_RNA /*tag= e
 FT misc_RNA 921. .2402
 FT misc_RNA /*tag= f
 FT misc_RNA 2403. .3464
 FT misc_RNA /*tag= g
 FT misc_RNA 3465. .4112
 FT misc_RNA /*tag= h
 FT misc_RNA 4113. .4499
 FT misc_RNA /*tag= i
 FT misc_RNA 4500. .6359
 FT misc_RNA /*tag= j
 FT misc_RNA 6300. .6809
 FT misc_RNA /*tag= k
 FT misc_RNA 6810. .7556
 FT misc_RNA /*tag= l
 FT misc_RNA 7557. .10268
 FT misc_RNA /*tag= m
 XX PN WO9322440-A1.

XX DR WPI; 1993-368799/46.
 DR P-PDB; AAR43362.
 XX PT New Dengue virus type 1 strain - used to obtain prods for detection,
 diagnosis, vaccines and treatment involving virus.
 XX PT
 XX PS Claim 3; Page 20-34; 55pp; English.

XX CC DEN1 virus, strain S275/90 was isolated from the serum of a dengue
 haemorrhagic fever (DHF) patient. RNA was isolated from the virus and
 used to prepare cDNA encoding DEN1 polypeptides. Dengue Virus Type 1
 prods. can be used for detection, diagnosis, vaccines (inactivated form)
 or treatment of DEN1 infections. The sequences given in AAQ5147-86 are
 oligonucleotides used to prepare cDNA fragments correld. to Dengue virus
 proteins by PCR. (Updated on 25-MAR-2003 to correct RN field.) (Updated
 on 27-AUG-2003 to correct OS field.)

SQ Sequence 10718 BP; 3419 A; 2226 C; 2769 G; 2304 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4%; DB 2; Length 10718;
 Best Local Similarity 96.4%; Pred. No. 0.07;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGGAGAGAACCCCG 28
 Db 120 AATATGCTGAAACGGAGAGAACCCCG 147

RESULT 25
 ID AAD14603 standard; cDNA; 10723 BP
 XX AC AAD14603;
 XX DT 11-BBP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX DE Dengue virus (DEN)-2/1-VP chimeric cDNA.
 XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
 XX OS Dengue virus; type I.
 OS Dengue virus; type II.
 OS Chimeric.
 XX FH Key Location/Qualifiers
 CDS 97. .10272
 FT FT /*tag= a
 FT FT /product= "DEN-2/1-VP fusion protein"
 FT FT WO200160847-A2.
 XX PN PR 16-FEB-2000; 2000US-0182829P.
 XX PD 23-AUG-2001.
 XX PP 16-FEB-2001; 2001WO-US005142.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvi N;
 XX DR WPI; 2001-497162/54.
 DR P-PDB; AAE01982.
 XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX PS Example 1; Page 155-170; 470pp; English.
 XX PI The invention relates to avirulent, immunogenic flavivirus chimeras

comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (NS3)-250 and the capsid protein (C), premembrane/membrane protein (prM) and an envelope protein (E) from wild-type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 10723 BP; 3514 A; 2229 C; 2722 G; 2258 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4%; DB 4; Length 10723;
Best Local Similarity 96.4%; Pred. No. 0.071;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGTTGAACGGAGAGAACCGCG 28
Db 136 AATATGTTGAACGGAGAGAACCGCG 163

RESULT 26

AAD11604 standard; cDNA; 10723 BP.
XX AC AAD11604;

XX DT 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)

DB Dengue virus (DEN)-2/1-VV chimeric cDNA.

XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; mutant; immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX Dengue virus; type I.
OS Dengue virus; type II.
OS Chimeric.

XX Key Location/Qualifiers

FT 97.10272

FT /*tag= a
FT /product= "DEN-2/1-VV fusion protein"

XX PN WO200160847-A2.

XX PD 23-AUG-2001.

XX PF 16-FEB-2001; 2001WO-US005142.

XX PR 16-FEB-2000; 2000US-0182829P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhama Pravati N;

XX DR 2001-497162/54.

DR P-PSDB; AAE07983.

XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
XX PS Example 1; Page 179-195; 470pp; English.
XX CC The invention relates to avirulent, immunogenic flavivirus chimeras

CC comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (NS3)-250 and the capsid protein (C), premembrane/membrane protein (prM) and an envelope protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3514 A; 2228 C; 2722 G; 2259 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4%; DB 4; Length 10723;
Best Local Similarity 96.4%; Pred. No. 0.071;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGTTGAACGGAGAGAACCGCG 28
Db 136 AATATGTTGAACGGAGAGAACCGCG 163

RESULT 27

AAD11602 standard; cDNA; 10735 BP.
XX AC AAD11602;

XX DT 01-NOV-2001 (first entry)

DB Attenuated, vaccine-strain DEN-1 PDK-13 variant cDNA.
XX Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; mutant; avirulent; immunogenic; viral disease; pharmaceutical; variant; ss.
XX Dengue virus; type I.
OS Synthetic.

XX Key Location/Qualifiers

FT 95.10273

FT /*tag= a
FT /product= "DEN-1 PDK-13 protein variant"
FT replace(1323, T)

FT /*tag= b
FT replace(1541, G)

FT /*tag= c
FT replace(1543, A)

FT /*tag= d
FT replace(1545, G)

FT /*tag= e
FT replace(1567, A)

FT /*tag= f
FT replace(1608, C)

FT /*tag= g
FT replace(2363, A)

FT /*tag= h
FT replace(2695, T)

FT /*tag= i
FT replace(2782, C)

FT /*tag= j
FT replace(5063, G)

FT /*tag= k
FT replace(6048, A)

FT /*tag= l
FT replace(6806, A)

PN WO2004040263-A2.
 XX DR WPI; 2000-679646/66.
 PD XX
 XX PT Novel compositions comprising tetracycline or tetracycline-like compounds
 PF 31-OCT-2003; 2003WO-US034423.
 XX PT for the treatment and/or prevention of acute inflammatory responses and
 PR 31-OCT-2002; 2002US-0422755P.
 PR PT diseases, e.g. septic shock and immune complex-induced colitis.
 PR 06-JUN-2003; 2003US-0476513P.
 XX PS Example 2; Page 103; 183pp; English.
 PA XX
 (HEAL-) HEALTH RES INC.
 XX
 PI Wong SJ, Pei-Yong S;
 XX
 DR WPI; 2004-400223/37.
 GENBANK; U88535.
 XX
 PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein
 PT reactive with antibody against WNV and cross-reactive with antibody
 PT against a flavivirus useful in diagnosing flavivirus infection caused by
 PT DENV, WNV, JEV or SLEV.
 XX
 Disclosure; Fig 39; 212pp; English.
 XX
 The invention relates to a diagnostic kit comprising at least one
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
 CC envelope (E) protein or its immunogenic fragment having a native
 CC conformation or non-denatured structure and that is reactive with
 CC antibodies against WNV and cross-reactive with antibodies against a
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
 CC the complete nucleotide sequence of the DENV isolate WestPac.
 XX
 Sequence 10735 BP; 3421 A; 2245 C; 274 G; 2295 T; 0 U; 0 Other;
 SQ Query Match 94.3%; Score 26.4%; DB 12; Length 10735;
 Best Local Similarity 96.4%; Pred. No. 0.071;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGAGAAACCGCG 28
 Db 134 AATATGCTGAAACGGAGAAACCGCG 161
 SQ
 RESULT 31
 AAT7517
 ID AAT7517 standard; DNA; 28 BP.
 XX
 AC AAT7517;
 XX DT 15-SEP-1997 (first entry)
 DE DEN-2 cloning/sequencing sense primer, D2-134.
 XX
 AAC68744
 ID AAC68744 standard; DNA; 26 BP.
 XX Dengue 2 virus; polyprotein; capsid; prM; E; NS1; NS2A; NS2B; NS3;
 AAC68744; NS4A; NS4B; NSS; PDK-53; quadrivalent vaccine; immunity; serotype;
 XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 DT DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
 XX OS Synthetic.
 DE DEN-2 upper primer.
 XX
 KW Dengue virus; antiinflammatory; haemostatic; antibacterial; sepsis;
 KW immuno-modulator; immunomodulator; cardiotonic; cytostatic; cachexia;
 KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
 KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
 KW chronic myelogenous leukaemia; inflammatory bowel disease; PCR primer;
 KW ss.
 XX
 OS Dengue virus.
 PN WO200064479-A1.
 XX
 PD 02-NOV-2000.
 XX PP 26-APR-2000; 2000WO-US011700.
 XX PR 27-APR-1999; 99US-00301274.
 XX
 (ANTI-) ANTIBODY SYSTEMS INC.
 XX
 Fredeking TM, Ignatyev GM;

XX WPI; 2000-679646/66.
 XX
 XX PT Novel compositions comprising tetracycline or tetracycline-like compounds
 PT for the treatment and/or prevention of acute inflammatory responses and
 PT diseases, e.g. septic shock and immune complex-induced colitis.
 XX PS Example 2; Page 103; 183pp; English.
 XX
 The present sequence was used in an invention relating to novel
 CC compositions and methods containing tetracycline or tetracycline-like
 CC compounds for treating and/or preventing acute inflammatory responses and
 CC diseases. Such diseases include inflammatory conditions associated
 CC with viral hemorrhagic diseases (including diseases caused by
 CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae),
 CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
 CC disorders, acute cardiovascular events, chronic myelogenous leukaemia and
 CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
 CC immune complex-induced colitis, cerebrospinal fluid inflammation,
 CC multiple sclerosis, inflammatory responses associated with trauma,
 CC systemic inflammatory response syndrome (SIRS), adult respiratory
 CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
 CC and Crohn's disease
 XX Sequence 26 BP; 11 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 SQ Query Match 92.9%; Score 26; DB 3; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.051.
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGAGAAACCG 26
 Db 1 AATATGCTGAAACGGAGAAACCG 26

RESULT 31
 AAT7517
 ID AAT7517 standard; DNA; 28 BP.
 XX
 AC AAT7517;
 XX DT 15-SEP-1997 (first entry)
 DE DEN-2 cloning/sequencing sense primer, D2-134.
 XX
 AAC68744
 ID AAC68744 standard; DNA; 26 BP.
 XX Dengue 2 virus; polyprotein; capsid; prM; E; NS1; NS2A; NS2B; NS3;
 AAC68744; NS4A; NS4B; NSS; PDK-53; quadrivalent vaccine; immunity; serotype;
 XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 DT DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
 XX OS Synthetic.
 XX WO964933-A1.
 PN WO964933-A1.
 XX
 AAC68744
 ID AAC68744 standard; DNA; 26 BP.
 XX PD 19-DEC-1996.
 AAC68744; XX DR
 XX PP 06-JUN-1996; 96WO-US006209.
 XX PR 07-JUN-1995; 95US-00483292.
 XX
 (USISH) US DEPT HEALTH & HUMAN SERVICES.
 PA (UWMA) UNIV MAHIDOL AT SALAYA.
 PA
 PI Bhamarapravati N, Butrapet S, Chang J, Gabler DJ, Halstead SB;
 PI Kinney R, Trent DW;
 XX DR
 XX WPI; 1997-052330/05.
 XX
 AAC68744
 ID AAC68744 standard; DNA; 26 BP.
 XX PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
 PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
 PT quadrivalent vaccine for protecting against Dengue virus infection.
 XX

PS Example; Page 100; 261pp; English.
 XX The sequences given in AAT75909-RT7609 are primers which were used in the amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the invention. The Dengue 2 viral DNA encodes a polyprotein which comprises the capsid, prM, M, E, NS1, NS2A, NS3, NS2B, NS4A, NS4B and NS5 proteins. The quadrivalent vaccine of the invention comprises an attenuated Dengue virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus. The new quadrivalent vaccines are used to protect against infection by all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used to produce the recombinant protein products of the DNA constructs which are used in the vaccines

XX Sequence 28 BP; 11 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 92.9%; Score 26; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.051; Matches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGCGAGAGAACCCG 26
 2 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 3 AATATGCTGAAACGGCGAGAGAACCCG 28

RESULT 32

AADI4610 ID AADI4610 standard; cDNA; 10699 BP.
 XX AC AADI4610;
 XX DT 11-SEP-2003 (revised)
 XX DE Wild-type, virulent DEN-3 16562 cDNA.

XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal; avirulent; immunogenic; viral disease; pharmaceutical; ss.
 XX Dengue virus; type III.
 XX Key Location/Qualifiers
 FH 95. .10267
 FT /*tag= a
 FT /product= "DEN-3 16562 protein"
 XX PN WO200160847-A2.
 XX PD 23-AUG-2001.
 XX PP 16-FBB-2001; 2001WO-US005142.
 XX PR 16-FBB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N; WPI; 2001-497162/54.
 XX DR P-PSDB; AAB07989.
 XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccination against a range of dengue viruses.
 XX PS Example 2; Page 325-341; 470pp; English.

CC The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the

CC accompanying clinical symptoms of viral disease. Attenuated chimeric CC flaviviruses are combined in a pharmaceutical composition to confer CC simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic CC flavivirus chimeras are also used as immunogens or multivalent vaccines CC to confer simultaneous protection against infections. The present cDNA CC sequence encodes wild-type, virulent dengue-3 (DEN-3) 16562 virus protein CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1 CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome CC contains 5' non-coding region followed by a capsid protein (C) encoding CC region, premembrane/membrane protein (prM) encoding region, an envelope CC protein (E) encoding region, followed by the region encoding non- CC structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3' CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 10699 BP; 3437 A; 2224 C; 2779 G; 2259 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 4; Length 10699;
 Best Local Similarity 92.9%; Pred. No. 0.37;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGCGAGAGAACCCG 28
 Db 134 AATATGCTGAAACGGCGAGAGAACCCGTG 161

RESULT 33

AADI4611 ID AADI4611 standard; cDNA; 10699 BP.
 XX AC AADI4611;
 XX DT 01-NOV-2001 (first entry)

XX DE Attenuated, vaccine-strain DEN-3 PGMK-30/FRLH-3 variant cDNA.
 XX KW Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal; mutant; variant; ss.
 XX OS Dengue virus; type III.
 XX OS Synthetic.

XX FH Key
 FT CDS
 FT /*tag= a
 FT /product= "DEN-3 PGMK-30/FRLH-3 protein variant"
 FT mutation
 FT FT
 FT /*tag= b
 FT replace(550, C)
 FT mutation
 FT FT
 FT /*tag= c
 FT replace(1838, A)
 FT /*tag= d
 FT replace(1913, G)
 FT mutation
 FT FT
 FT /*tag= e
 FT replace(2140, C)
 FT mutation
 FT FT
 FT /*tag= f
 FT replace(3725, T)
 FT mutation
 FT FT
 FT /*tag= g
 FT replace(4781, C)
 XX PN WO200160847-A2.
 XX PD 23-AUG-2001.

XX PP 16-FBB-2001; 2001WO-US005142.
 XX PR 16-FBB-2000; 2000US-0182829P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N; WPI; 2001-497162/54.
 XX DR P-PSDB; AAB07989.
 XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccination against a range of dengue viruses.
 XX PS Example 2; Page 325-341; 470pp; English.

CC The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the

XX SQ Sequence 10699 BP; 3437 A; 2224 C; 2779 G; 2259 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 4; Length 10699;
 Best Local Similarity 92.9%; Pred. No. 0.37;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGCGAGAGAACCCG 28
 Db 134 AATATGCTGAAACGGCGAGAGAACCCGTG 161

RESULT 34

AADI4611 ID AADI4611 standard; cDNA; 10699 BP.
 XX AC AADI4611;

XX DT 01-NOV-2001 (first entry)

XX DE Attenuated, vaccine-strain DEN-3 PGMK-30/FRLH-3 variant cDNA.
 XX KW Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal; mutant; variant; ss.
 XX OS Dengue virus; type III.
 XX OS Synthetic.

XX FH Key
 FT CDS
 FT /*tag= a
 FT /product= "DEN-3 PGMK-30/FRLH-3 protein variant"
 FT mutation
 FT FT
 FT /*tag= b
 FT replace(550, C)
 FT mutation
 FT FT
 FT /*tag= c
 FT replace(1838, A)
 FT /*tag= d
 FT replace(1913, G)
 FT mutation
 FT FT
 FT /*tag= e
 FT replace(2140, C)
 FT mutation
 FT FT
 FT /*tag= f
 FT replace(3725, T)
 FT mutation
 FT FT
 FT /*tag= g
 FT replace(4781, C)
 XX PN WO200160847-A2.
 XX PD 23-AUG-2001.

XX PP 16-FBB-2001; 2001WO-US005142.
 XX PR 16-FBB-2000; 2000US-0182829P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

xx	Sequence 10699 BP:	3439 A;	2221 C;	2778 G;	2261 T;	0 U;	0 Other;
sq	Query Match	88.6%	Score 24.8;	DB 4;	Length 10699;		
	Best Local Similarity	92.9%	Pred. No. 0.37;				
	Matches 25;	Conservative	0; Mismatches 2;	Indels 0;	Gaps		
Qy	1	AATATGCTGAAACCGAGAGAACCGCG	28				
	1134	AATATGCTGAAACCGTGGAAAACCGTG	161				
db							

RESULT	34
ID	ADG93315 standard; DNA; 15153 BP.
XX	ADG93315;
AC	
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	DEN3 (St. Leeman/78) cDNA plasmid p3.
XX	
KW	immunogenic composition; dengue type 1; dengue type 2; dengue type 3
KW	dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine
KW	dengue virus; delta30; attenuating mutation; humoral response;
KW	cellular response; non-structural protein; structural protein;
KW	dengue virus serotype; gene; ds; plasmid p3.
XX	
OS	Dengue virus type 3.
XX	

Hanley K;
WPI: 2004-022612/02.
P-PSDBB; ADG93316.

New tetravalent vaccine containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4, useful for preventing disease in humans caused by dengue virus, or for inducing immune response.

Disclosure: SEQ ID NO 48; 181pp; English.

This invention relates to a novel immunogenic composition being tetraivalent and containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4. The invention may be useful for the development of compounds with a virucide or immunostimulant activity or as a vaccine. The tetravalent vaccine is useful in the prevention of disease in humans caused by dengue virus. Unlike previous tetravalent vaccine, the new tetravalent vaccine is unique since they contain a common shared attenuating mutation which eliminates the possibility of generating a virulent wild type virus in a subject to be vaccinated since each component of the vaccine possesses the same delta30 attenuating deletion mutation. The vaccine also is able to induce humoral and cellular responses against all of the (non-structural) proteins present in each dengue virus serotype. The present sequence is that of the DEN3 cDNA plasmid P3 which is related to the invention.

Sequence 15153 BP; 4434 A; 3440 C; 3336 T; 0 U; 0 Other;
 Query Match 88.6%; Score 24.8; DB 12; Length 15153;
 Best Local Similarity 92.9%; Pred. No. 0.39;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1 AATATGCTGAAACGGAGAACCGGG 28
 ||||| ||||| ||||| ||||| ||||| |||||
 134 AATATGCTGAAACGGTGTGAGAACCGTG 161

JLT 35
 38836
 AAF88836 standard; DNA; 72 BP.
 AAF88836;
 09-JAN-2003 (first entry)

Green fluorescent protein PCR primer #1.
 Replicon; structural region; vaccine; subgenomic replicon; gene therapy;
 structural protein; C protein; PCR primer; 3' protein;
 GFP; green fluorescent protein; PCR primer; aa

immunogenic composition; dengue type 1; dengue type 2; dengue type 3
dengue type 4; viruside; immunostimulant; vaccine; tetravalent vaccine;
dengue virus; delta30; attenuating mutation; humoral response;
cellular response; non-structural protein; structural protein;

הנתקה בראבּוֹן וְבָרְבָּרָן

S Example 3: Page 38; 660B; English

S	S	Example 2; Page 38; 66pp; English.	99US-0132863P.
X	X	This invention describes a novel subgenomic replicon of dengue virus origin comprising a deletion for the sequence coding for C, PREM and E (DeTAcME), or for E (DeTAIE) structural proteins, and/or which is adapted to receive at least a nucleotide sequence without disrupting its replication capabilities. The products of the invention can be used for constructing (1) a vaccine or a therapeutic comprising the subgenomic replicon and a carrier; (2) a dengue virus-like particle comprising the subgenomic replicon, and structural proteins of the homologous dengue virus, which encapulates the subgenomic replicon; and (3) methods of immunisation and treatment comprising administering to the individual the subgenomic replicon or the dengue virus like particle cited above. The subgenomic replicons are useful in gene therapy as vaccines for immunisation against dengue virus infection. This sequence represents a PCR primer used with AAF8837 to amplify the green fluorescent protein (GFP) gene cloned into the dengue virus deltarep-M/E replicon, at the site previously occupied by the pre-M/E genes	99US-0132863P.
X	X	Sequence 72 BP; 26 A; 12 C; 24 G; 10 T; 0 U; 0 Other;	99US-0132863P.
X	X	Query Match 78.6%; Score 22; DB 6; Length 72;	99US-0132863P.
X	X	Best Local Similarity 100.0%; Pred. No. 3.7;	99US-0132863P.
X	X	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	99US-0132863P.
b	b	1 AATATGCTGAAACGGAGAGAA 22 28 AATATGCTGAAACGGAGAGAA 49	99US-0132863P.
RESULT 36			
D	D	AAC44997/C	99US-0132863P.
X	X	Arabidopsis thaliana DNA fragment SEQ ID NO: 44912.	99US-0132863P.
C	C	AAC44997;	99US-0132863P.
T	T	18-OCT-2000 (first entry)	99US-0132863P.
X	X	Arabidopsis thaliana DNA fragment SEQ ID NO: 44912.	99US-0132863P.
X	X	Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.	99US-0132863P.
X	X	Arabidopsis thaliana.	99US-0132863P.
S	S	EP1033405-A2.	99US-0132863P.
N	N	06-SEP-2000.	99US-0132863P.
X	X	25-FEB-2000; 2000EP-00301439.	99US-0132863P.
X	X	25-FEB-1999; 99US-0121825P.	99US-0132863P.
R	R	05-MAR-1999; 99US-012310P.	99US-0132863P.
R	R	09-MAR-1999; 99US-0123548P.	99US-0132863P.
R	R	23-MAR-1999; 99US-0125788P.	99US-0132863P.
R	R	25-MAR-1999; 99US-0126264P.	99US-0132863P.
R	R	29-MAR-1999; 99US-0126785P.	99US-0132863P.
R	R	01-APR-1999; 99US-01274162P.	99US-0132863P.
R	R	06-APR-1999; 99US-0128234P.	99US-0132863P.
R	R	08-APR-1999; 99US-0128714P.	99US-0132863P.
R	R	16-APR-1999; 99US-0129845P.	99US-0132863P.
R	R	19-APR-1999; 99US-0130077P.	99US-0132863P.
R	R	21-APR-1999; 99US-0130449P.	99US-0132863P.
R	R	23-APR-1999; 99US-0130510P.	99US-0132863P.
R	R	23-APR-1999; 99US-0130891P.	99US-0132863P.
R	R	28-APR-1999; 99US-0131449P.	99US-0132863P.
R	R	30-APR-1999; 99US-0132048P.	99US-0132863P.
R	R	04-MAY-1999; 99US-0132484P.	99US-0132863P.
R	R	05-MAY-1999; 99US-0132485P.	99US-0132863P.
R	R	06-MAY-1999; 99US-0132486P.	99US-0132863P.
R	R	06-MAY-1999; 99US-0132487P.	99US-0132863P.

PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	26-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145911P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161922P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161933P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0161424P.
PR	04-AUG-1999;	99US-0147192P.			
PR	05-AUG-1999;	99US-0147260P.	Query Match	68 6%;	Score 19.2;
PR	06-AUG-1999;	99US-0147261P.	Best Local Similarity	87.5%;	Pred. No. 93;
PR	06-AUG-1999;	99US-0147416P.	Matches	21;	Mismatches
PR	09-AUG-1999;	99US-0147419P.	2	ATATGCTGAAACGGAGAGAACC 25	3;
PR	10-AUG-1999;	99US-0147335P.	3.4	ATATGCTGAAACGGAGAGAAC 11	Indels
PR	11-AUG-1999;	99US-0148171P.	0;		Gaps
PR	12-AUG-1999;	99US-0148319P.			
PR	13-AUG-1999;	99US-0148365P.	RESULT	37	
PR	16-AUG-1999;	99US-0148684P.	ID	ADL98061	standard; DNA; 19 BP.
PR	17-AUG-1999;	99US-0149175P.	XX		
PR	18-AUG-1999;	99US-0149426P.	AC	ADL98061;	
PR	20-AUG-1999;	99US-0149722P.	XX		
PR	20-AUG-1999;	99US-0149723P.	DT	03-JUN-2004	(first entry)
PR	23-AUG-1999;	99US-0149929P.	XX		
PR	23-AUG-1999;	99US-0149368P.	DB	SCRO gene specific PCR primer SEQ ID NO:6.	
PR	25-AUG-1999;	99US-0150565P.	XX		
PR	26-AUG-1999;	99US-0150884P.	KW	Strand specific amplification; convertible oligonucleotide;	
PR	27-AUG-1999;	99US-0151065P.	KW	multi-conformational chimeric nucleotide; hemi-nested primer; detection;	
PR	27-AUG-1999;	99US-0151065P.	KW	quantification; identification; drug evaluation; viral replication inhibition; PCR primer; ss.	
PR	30-AUG-1999;	99US-0151303P.	KW		
PR	31-AUG-1999;	99US-0151313P.	XX		
PR	01-SEP-1999;	99US-0151940P.	OS		
PR	07-SEP-1999;	99US-0152363P.	XX		
PR	10-SEP-1999;	99US-0153070P.	XX		
PR	13-SEP-1999;	99US-0153758P.	XX		
PR	15-SEP-1999;	99US-0154018P.	XX		
PR	16-SEP-1999;	99US-0154030P.	XX		
PR	20-SEP-1999;	99US-0154779P.	XX		
PR	22-SEP-1999;	99US-0155139P.	XX		
PR	23-SEP-1999;	99US-0155486P.	XX		
PR	24-SEP-1999;	99US-0155659P.	XX		
PR	28-SEP-1999;	99US-0156458P.	XX		
PR	29-SEP-1999;	99US-0156536P.	XX		
PR	04-OCT-1999;	99US-0157117P.	XX		
PR	05-OCT-1999;	99US-0157533P.	XX		
PR	06-OCT-1999;	99US-0157533P.	XX		
PR	07-OCT-1999;	99US-0158059P.	XX		
PR	08-OCT-1999;	99US-0158332P.	XX		
PR	12-OCT-1999;	99US-0158359P.	XX		
PR	13-OCT-1999;	99US-0159233P.	PS	Disclosure; SEQ ID NO 6; 79pp; English.	
PR	13-OCT-1999;	99US-0159294P.	XX		
PR	14-OCT-1999;	99US-0159255P.	CC	The present invention describes a strand specific amplification method which comprises: (a) determining nucleic acid sequences of a target nucleic acid strand; (b) designing a convertible oligonucleotide based, at least in part, on the target nucleic acid strand; (c) conducting a transcription reaction utilising the convertible oligonucleotide and the target nucleic acid strand to prove at least one resultant complementary strand; (d) conducting an amplification reaction to amplify the at least one resultant complementary strand; and (e) analysing the amplification reaction. Also described: (1) a convertible oligonucleotide comprising a first self-annealing portion and a second portion complementary at least in part, to a target nucleic acid sequence; and (2) designing multi-conformational chimeric nucleotides and hemi-nested primers. The method is useful for strand specific amplification. The method is useful in	
PR	14-OCT-1999;	99US-0159310P.	CC		
PR	14-OCT-1999;	99US-0159637P.	CC		
PR	18-OCT-1999;	99US-0159638P.	CC		
PR	21-OCT-1999;	99US-0160741P.	CC		
PR	21-OCT-1999;	99US-0160767P.	CC		
PR	21-OCT-1999;	99US-0160768P.	CC		
PR	21-OCT-1999;	99US-0160770P.	CC		
PR	21-OCT-1999;	99US-0160814P.	CC		
PR	21-OCT-1999;	99US-0160815P.	CC		

CC detecting and quantifying nucleic acids, detecting and identifying
 CC pathogens and in evaluating drugs that inhibit viral replication. The
 CC present sequence is used in the exemplification of the present invention.

XX Sequence 19 BP; 8 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
 SQ Score 19; DB 12; Length 19;
 Query Match 67.9%; Best Local Similarity 100.0%; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 TGAACGCGAGAGAACCG 26
 Db 1 TGAACGCGAGAGAACCG 19

RESULT 38 ABQ14003 standard; DNA; 765 BP.

ID ABQ14003

XX AC ABQ14003;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20594.

XX DB Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX KW drug; side effect; cancer; central nervous system; cardiovascular;

XX KW gastrointestinal; respiratory system; single nucleotide polymorphism;

XX SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO200218632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PR 05-SEP-2000; 2000DE-01043826.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX PT Determining the degree of cytosine methylation in genomic DNA, useful for
 diagnosis and prognosis, comprises selective hybridization of amplicons
 from chemically treated DNA.

XX DR WPI; 2002-371829/40.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX CC This invention describes a novel method for determining the degree of
 methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 genomic sample of DNA. The sample is treated chemically to convert
 cytosine (C) but not methylated C, to uracil, then part of the genomic
 DNA that contains the target C is amplified to form a labeled amplicon.

CC The amplicon is hybridised to two classes, each with at least one member,

CC of oligonucleotides and/or peptide-nucleic acid (PNA) Oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ14121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention

CC Sequence 765 BP; 119 A; 80 C; 230 G; 336 T; 0 U; 0 Other;

CC SQ

XX Sequence 765 BP; 336 A; 230 C; 80 G; 119 T; 0 U; 0 Other;

SQ Query Match 67.9%; Score 19; DB 6; Length 765;

XX Best Local Similarity 81.5%; Pred. No. 1.1e+02;

XX Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGGAGAACCG 28

Db 441 ATACCCGAAACGGAACGAAACGG 467

XX RESULT 39 ABQ14002/C

XX ID ABQ14002 standard; DNA; 765 BP.

XX AC ABQ14002;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20593.

XX DB Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX KW drug; side effect; cancer; central nervous system; cardiovascular;

XX KW gastrointestinal; respiratory system; single nucleotide polymorphism;

XX SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO2018632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX CC This invention describes a novel method for determining the degree of
 methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 genomic sample of DNA. The sample is treated chemically to convert
 cytosine (C) but not methylated C, to uracil, then part of the genomic
 DNA that contains the target C is amplified to form a labeled amplicon.

CC The amplicon is hybridised to two classes, each with at least one member,

CC of oligonucleotides and/or peptide-nucleic acid (PNA) Oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ14121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention

CC Sequence 765 BP; 119 A; 80 C; 230 G; 336 T; 0 U; 0 Other;

CC SQ

Query Match Score 19; DB 6; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 5;
Indels 0; Gaps 0;

RESULT 40
ADD46068 ADD46068 standard; DNA; 28564 BP.
XX

QY 2 ATATGCTGAAACGGAGAGAAACCGCG 28
Db 325 ATACCCGAAACGGCAACAAAACCG 299

RESULT 40
ADD46068 ADD46068 standard; DNA; 28564 BP.
XX

29-JAN-2004 (first entry)
Human Gene AL138478, SEQ ID NO 11743.
XX

Human; ds; gene; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
XX

Homo sapiens.
XX

WO2003016475-A2.
27-FEB-2003.
XX

14-AUG-2002; 2002W0-US005765.
XX

14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0316382P.
26-NOV-2001; 2001US-0333347P.
XX

(GBHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX

WOLF C, D'URSO D, BEFORT K, COSTIGAN M;
WPI; 2003-268312/26.
GENBANK; AL138478.

New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
XX

Claim 1; Page: 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides or their antibodies. The pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in creating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human DNA (shown in Table 2 of the specification) which encodes one of the polypeptides of the invention which is differentially expressed during pain. Note: The sequence data

PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0147171P.
PR	14-JUN-1999;	99US-0139119P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148365P.
PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-014975P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	99US-0139461P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139462P.	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	99US-0139457P.	PR	27-AUG-1999;	99US-015065P.
PR	18-JUN-1999;	99US-0139463P.	PR	27-AUG-1999;	99US-015066P.
PR	18-JUN-1999;	99US-0139458P.	PR	27-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	99US-0139459P.	PR	23-AUG-1999;	99US-0149903P.
PR	21-JUN-1999;	99US-0139460P.	PR	23-AUG-1999;	99US-0149930P.
PR	22-JUN-1999;	99US-0139461P.	PR	25-AUG-1999;	99US-015066P.
PR	23-JUN-1999;	99US-0139462P.	PR	26-AUG-1999;	99US-0150884P.
PR	23-JUN-1999;	99US-0139463P.	PR	27-AUG-1999;	99US-0151065P.
PR	24-JUN-1999;	99US-0139750P.	PR	20-AUG-1999;	99US-0151066P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0149929P.
PR	21-JUN-1999;	99US-0139817P.	PR	23-AUG-1999;	99US-0149931P.
PR	22-JUN-1999;	99US-0139899P.	PR	23-AUG-1999;	99US-0149930P.
PR	23-JUN-1999;	99US-0140353P.	PR	31-AUG-1999;	99US-0151438P.
PR	01-JUL-1999;	99US-0140354P.	PR	01-SEP-1999;	99US-0151930P.
PR	02-JUL-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-0151363P.
PR	06-JUL-1999;	99US-0140823P.	PR	10-SEP-1999;	99US-0153070P.
PR	08-JUL-1999;	99US-0140991P.	PR	13-SEP-1999;	99US-0153758P.
PR	09-JUL-1999;	99US-0141287P.	PR	15-SEP-1999;	99US-0154018P.
PR	12-JUL-1999;	99US-0141842P.	PR	16-SEP-1999;	99US-0154039P.
PR	13-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.
PR	14-JUL-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-015139P.
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-015486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-015458P.
PR	12-JUL-1999;	99US-0143277P.	PR	29-SEP-1999;	99US-015569P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-015753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	19-JUL-1999;	99US-0144334P.	PR	08-OCT-1999;	99US-0158232P.
PR	20-JUL-1999;	99US-0144335P.	PR	12-OCT-1999;	99US-0158369P.
PR	20-TUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	20-TUL-1999;	99US-0144632P.	PR	13-OCT-1999;	99US-0159294P.
PR	21-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	22-JUL-1999;	99US-0144325P.	PR	14-OCT-1999;	99US-0159331P.
PR	22-JUL-1999;	99US-0144632P.	PR	21-OCT-1999;	99US-016070P.
PR	22-JUL-1999;	99US-0144884P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0144914P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145244P.	PR	22-OCT-1999;	99US-0161768P.
PR	26-JUL-1999;	99US-0145085P.	PR	25-OCT-1999;	99US-0161404P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145130P.	PR	27-OCT-1999;	99US-0161359P.
PR	27-JUL-1999;	99US-0145192P.	PR	28-OCT-1999;	99US-0161360P.
PR	28-JUL-1999;	99US-0145919P.	PR	28-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0145951P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146386P.	PR	28-OCT-1999;	99US-0161922P.
PR	03-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161933P.
PR	04-AUG-1999;	99US-0147038P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162144P.

Query Match 67.1% ; Score 18.8 ; DB 3 ; Length 1008 ;

PN US2002142407-A1.
 XX
 PD 03-OCT-2002.
 XX
 PP 09-JAN-2002; 2002US-00042991.
 XX
 PR 24-MAY-2000; 2000US-00578533.
 PA (FIRM) FIRMENICH SA.
 XX
 Whitehead IM, Slusarenko AJ, Waspi U, Gaskin DJH, Brash AR;
 PT Tijet N;
 PI DR; DR-PSDB; ABG74402.
 XX
 PT Cleaving 13-hydroperoxide of linoleic acid into aldehyde and
 PT oxocarboxylic acid, and preparing n-hexanal from 13-hydroperoxy-octadeca-
 PT 9,11-dienoic acid, using recombinant fatty acid 13-hydroperoxide lyase.
 XX
 Disclosure: Page 21-22; 35pp; English.
 PS Sequence 1443 BP; 418 A; 288 C; 295 G; 442 T; 0 U; 0 Other;
 CC The invention describes a method of cleaving 13-hydroperoxide (I) of
 CC linoleic or alpha-linolenic acid into 6C-aldehyde (A) and 12C-
 CC oxocarboxylic acid (B). The method involves the use of recombinant
 CC protein produced by a vector containing nucleic acid encoding fatty acid
 CC 13-hydroperoxide lyase (HPL). The method is useful for cleaving 13-
 CC hydroperoxide of linoleic or alpha-linolenic acid into a 6C-aldehyde and
 CC a 12C-oxocarboxylic acid, and for preparing n-hexanal, 3-(Z)-hexen-1-ol,
 CC 2-(E)-hexen-1-ol, 6C-aldehyde, 12C-oxocarboxylic acid, or their
 CC corresponding alcohols from 13-hydroperoxy-octadeca-9,11-dienoic acid or
 CC 13-hydroperoxy-octadeca-9,11,15-trienoic acid. This sequence sequence
 CC encodes green pepper 13-hydroperoxide lyase (13-HPL).
 XX
 SQ Sequence 1443 BP; 418 A; 288 C; 295 G; 442 T; 0 U; 0 Other;
 Query Match 65.7%; Score 18.4; DB 9; Length 1443;
 Best Local Similarity 78.6%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGCGAGAACCGCG 28
 Db 933 AAAATGCTGAGTGCAGAGAACACTGAG 960

RESULT 47
 ADF44354
 ID ADF44354 standard; DNA; 1647 BP.
 XX
 AC ADF44354;
 XX
 DT 12-FEB-2004 (first entry)
 DE 1647bp sense HPL gene from green pepper.
 XX
 KW transformed; transgenic plant; hydroperoxide lyase; HPL;
 KW volatile biosynthesis HPL enzyme; insect; extermination; isothiocyanate;
 KW agrochemical; gene; green pepper; ds.
 XX
 OS Capsicum annuum.
 PN JP2003339260-A.
 XX
 PD 02-DEC-2003.
 XX
 PP 27-MAY-2002; 2002JP-00153094.
 XX
 PR 27-MAY-2002; 2002JP-00153094.
 XX
 PA (KYOTO) UNIV KYOTO.
 XX
 DR WPI; 2004-039487/04.

PN Claim 3; SEQ ID NO 1; 20pp; Japanese.
 PS
 XX
 CC The invention relates to a novel transformed plant in which a
 CC hydroperoxide lyase (HPL) gene coding for a volatile biosynthesis HPL
 CC enzyme is transduced in the sense antisense direction, where activity of
 CC the HPL enzyme is improved or reduced compared to wild type plant. The
 CC invention further relates an insect-extermination method using the
 CC transformed plant. In the transformed plant, the HPL gene is transduced
 CC in the sense direction and has fully defined sequence of 1647 base
 CC pairs as given in the specification, and is derived from green pepper.
 CC The HPL gene transduced in the antisense direction has a fully defined
 CC sequence of 1711 base pairs as given in the specification, and is derived
 CC from *Arabidopsis thaliana*. The biosynthesis of an isothiocyanate compound
 CC is promoted in the transformed plant compared to the wild-type plant. The
 CC transformed plant is a Brassicaceae plant such as *A. thaliana*. The
 CC transformed plant efficiently terminates an insect pest and also
 CC effectively inhibits growth of an insect pest. The novel transformed
 CC plant reduces the usage of an agrochemical. This polynucleotide sequence
 CC represents the 1647bp HPL gene from a green pepper of the invention.
 XX
 SQ Sequence 1647 BP; 517 A; 314 C; 320 G; 496 T; 0 U; 0 Other;
 Query Match 65.7%; Score 18.4;
 Best Local Similarity 78.6%; Pred. No. 2.3e+02;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGCGAGAACCGCG 28
 Db 977 AAAATGCTGAGTGCAGAGAACACTGAG 1004

RESULT 48
 AAQ22767
 ID AAQ22767 standard; DNA; 4512 BP.
 XX
 AC AAQ22767;
 XX
 DT 12-AUG-1992 (first entry)
 DE JEV Nakayama strain prM, E, NS1, NS2A, NS2B and C coding regions.
 XX
 JP Japanese Encephalitis Virus; vaccinia virus donor; plasmid pDr20; 88.
 XX
 OS Japanese encephalitis virus.
 XX
 PN WO9203545-A.
 XX
 DT 05-MAR-1992.
 XX
 PP 05-AUG-1991; 91WO-US005816.
 XX
 PR 15-AUG-1990; 90US-00557960.
 PR 06-JUN-1991; 91US-00711429.
 PR 13-JUN-1991; 91US-00714687.
 PR 17-JUL-1991; 91US-00739800.
 PR 05-AUG-1991; 91WO-U0005816.
 XX
 (VIRO-) VIROGENETICS CORP.
 PI Paolatti E, Pinc, Pincus SE;
 XX
 DR WPI; 1992-096889/12.
 XX
 PT Recombinant pox-virus e.g. vaccinia, fowl-pox and canary-pox virus -
 PT contg. DNA from flavi-virus e.g. Japanese encephalitis and yellow fever
 XX
 PS Example 9; Fig 17; 117pp; English.
 XX

CC cDNA was prepared from genomic virion RNA obtained from suspension cultures of C6/36 cells infected with a passage 55 suckling mouse brain stock of the Nagayama strain of JEV. EcoRI linkers were ligated to the CC cDNA fragments for cloning into pBR322. Recombinant plasmids were transformed into E.coli DH5 cells. Plasmid pc20 contained 81 non-coding CC nucleotides and the coding regions for C and PRM. Sequence AAQ2276 is that of the C coding region of pc20, combined with an updated sequence of the PRM, E, NS1, NSSA and NS2B coding regions of the Nagayama strain. The sequence begins at the C protein Met initiation codon. A subfragment of pc20 was cloned into pUC18 to give pDR20. This plasmid was then used in the construction of novel recombinants JEV24, JEV27, JEV33 and JEV34. These were transfected into VP40 infected cells to generate vP825, vP829, vP857 and vP864, respectively.

SQ	Sequence 4512 BP; 1192 A; 1055 C; 1253 G; 1012 T; 0 U; 0 Other;	Qy	1 AATATGCTGAAACGGAGAGAAACCGCG 28
		Db	88 AATATGCTGAAACGGAGAGAAACCGCG 115
			RESULT 50
			ADO07437
			ID ADO07437 standard; DNA; 10968 BP.
			XX
			AC ADO07437;
			XX
			DT 15-JUL-2004 (first entry)
			XX
			DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 15.
			XX
			KW antiinflammatory; neuroprotective; gene therapy;
			KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;
			KW Japanese encephalitis.
			OS Japanese encephalitis virus.
			XX
			WO2004033690-A1.
			XX
			PN WO2004033690-A1.
			XX
			PP 09-OCT-2003; 2003WO-KR00061589.
			XX
			PR 09-OCT-2002; 2002KR-00061589.
			XX
			(CIDC-) CID CO LTD.
			PA (LEES/) LEE S H.
			XX
			PI Lee SH, Lee Y, Yun S;
			XX
			DR WPI; 2004-340933/31.
			XX
			PT New Japanese encephalitis virus genomic RNA, useful in developing vaccines for and in diagnosing and treating Japanese encephalitis.
			PT
			OS Claim 3; Page 154-161; 265pp; English.
			XX
			PS XX
			The present invention relates to a genomic RNA of the Korean Japanese Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated region (NTR) and a single polypeptide coding region. The JEV genomic RNA, JEV cDNA and reagents are useful in developing vaccines for and in diagnosing and treating Japanese encephalitis. The present sequence is a sequence of the invention.
			XX
			SQ Sequence 10968 BP; 3032 A; 2518 C; 3117 G; 2301 T; 0 U; 0 Other;
			XX
			Query Match Score 18.4%; Score 18.4%; DB 12; Length 10968;
			Best Local Similarity 78.6%; Pred. No. 2.8e+02;
			Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
			XX
			Qy 1 AATATGCTGAAACGGAGAGAAACCGCG 28
			DB 138 AATATGCTGAAACGGAGAGAAACCGCG 165
			XX
			Search completed: January 19, 2005, 13:12:16
			Job time : 206 secs
			XX
			The present invention relates to a genomic RNA of the Korean Japanese Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated region (NTR) and a single polypeptide coding region. The JEV genomic RNA, JEV cDNA and reagents are useful in developing vaccines for and in diagnosing and treating Japanese encephalitis. The present sequence is a sequence of the invention.
			XX
			SQ Sequence 10818 BP; 2991 A; 2491 C; 3075 G; 2261 T; 0 U; 0 Other;
			XX
			PS Example 2; Page 145-152; 265pp; English.
			XX
			The present invention relates to a genomic RNA of the Korean Japanese Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated region (NTR) and a single polypeptide coding region. The JEV genomic RNA, JEV cDNA and reagents are useful in developing vaccines for and in diagnosing and treating Japanese encephalitis. The present sequence is a sequence of the invention.
			XX
			PS Query Match Score 18.4%; Score 18.4%; DB 12; Length 10818;
			Best Local Similarity 78.6%; Pred. No. 2.8e+02;
			Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Result No.	Score	Query	Match	Length	DB	ID	Description
1	28	100.0	2357	4	US-08-669-433-1		Sequence 1, Appli
2	28	100.0	3381	3	US-08-937-195-1		Sequence 1, Appli
3	28	100.0	3381	3	US-08-937-195-2		Sequence 2, Appli
4	28	100.0	3381	3	US-08-915-152-1		Sequence 1, Appli
5	28	100.0	3381	3	US-08-915-152-2		Sequence 2, Appli
6	28	100.0	3381	4	US-08-937-1433-2		Sequence 2, Appli
7	28	100.0	3381	5	PCT-US96-07627-1		Sequence 1, Appli
8	28	100.0	3381	5	PCT-US96-07627-2		Sequence 2, Appli
9	26.4	94.3	10718	3	US-08-325-446B-1		Sequence 1, Appli
c 10	18.6	66.4	1145	4	US-09-270-767-981.9		Sequence 9819, Ap
11	18.4	65.7	1443	3	US-09-078-173A-11		Sequence 11, Appli
12	18.4	65.7	1443	4	US-10-04-991-11		Sequence 11, Appli
13	18.4	65.7	4512	1	US-08-224-391-52		Sequence 52, Appli
14	18.4	65.7	4512	1	US-08-484-304-52		Sequence 52, Appli
c 15	18.4	65.7	12980	3	US-08-811-566-5		Sequence 5, Appli
c 16	18.4	65.7	12980	3	US-09-034-756-5		Sequence 5, Appli
17	17.6	62.9	3351	4	US-09-583-110-2413		Sequence 2433, Ap
18	17.4	62.1	763	4	US-09-270-767-8006		Sequence 8086, Ap
19	17.4	62.1	763	4	US-09-770-767-23368		Sequence 23368, A
20	17.4	62.1	983	3	US-08-875-23-11		Sequence 11, Appli
c 21	17.4	62.1	1227	4	US-09-328-352-1888		Sequence 1888, Ap
c 22	17.4	62.1	2646	4	US-09-221-017B-555		Sequence 558, Ap
23	17.4	62.1	5026	4	US-09-549-872B-3		Sequence 3, Appli
24	17.4	62.1	6612	4	US-09-549-872B-5		Sequence 5, Appli
25	17.4	62.1	11207	4	US-09-549-872B-2		Sequence 2, Appli
c 26	17.2	61.4	3243	1	US-08-511-107-32		Sequence 32, Appli
27	17.2	61.4	24358	4	US-09-392-812A-1		Sequence 1, Appli

MOLECULE TYPE: RNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Dengue virus

STRAIN: New Guinea C

POSITION IN GENOME:

CHROMOSOME/SEGMENT: PreM and Envelope

MAP POSITION: 330-2446

UNITS: bp

PUBLICATION INFORMATION:

AUTHORS: Gruenberg, A

AUTHORS: Woo, W S

AUTHORS: Biedrzycka, A

AUTHORS: Wright, P J

TITLE: Partial nucleotide sequence and deduced amino acid sequence of the structural proteins of dengue virus type 2, New Guinea C and PVO-218 strains

JOURNAL: J. Gen. Virol.

VOLUME: 69

PAGES: 1391-1398

DATE: 1988

PUBLICATION INFORMATION:

AUTHORS: Irie, K

AUTHORS: Mohan, P M

AUTHORS: Sasaguri, Y

AUTHORS: Putnak, R

AUTHORS: Padmanabhan, R

TITLE: Sequence Analysis of Cloned dengue virus type

PATENT No: 6155509

TITLE: 2 genome (New Guinea-C strain)

JOURNAL: Gene

VOLUME: 75

ISSUE: 2

PAGES: 197-211

PUBLICATION INFORMATION:

AUTHORS: Yaegashi, T

AUTHORS: Vakharla, V N

AUTHORS: Page, K

AUTHORS: Sasaguri, Y

AUTHORS: Feijny, R

AUTHORS: Padmanabhan, R

JOURNAL: Gene

VOLUME: 46

ISSUE: 2-3

PAGES: 257-267

DATE: 1986

US-08-869-423-1

Query Match 100.0% Score 28; DB 4; Length 2357;
Best Local Similarity 100.0% Pred. No. 0.0011; Indels 0; Gaps 0;

Matches 28; Conservative 0; Mismatches 0; Feature:

QY 1 AATATCTGAAACGGAGAGAACCGCG 28
Db 60 AATATGCTGAAACGGAGAGAACCGCG 87

RESULT 2
US-08-937-195-1
Sequence 1, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500

FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: 343
 OTHER INFORMATION: /note= "Start of coding strand
 sequence for preMembrane"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 616
 OTHER INFORMATION: /note= "Start of coding strand
 sequence for Membrane"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 841
 OTHER INFORMATION: /note= "Start of coding strand
 sequence for Envelope"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 2326_
 OTHER INFORMATION: /note= "Start of coding strand
 sequence for NS1"
 PUBLICATION INFORMATION:
 AUTHORS: Hahn, Y.S.
 JOURNAL: Virology
 VOLUME: 162
 PAGES: 167-180
 DATE: 1988
 US-08-937-195-1
 Query Match 1 AATATGCTAAACGGAGAAAACCGCG 28
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 28; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Db 40 AATATGCTAAACGGAGAAAACCGCG 67

RESULT 3
 US-08-937-195-2
 Sequence 2, Application US/08937195
 Patent No. 6136561
 GENERAL INFORMATION:
 APPLICANT: IVY, JOHN M.
 APPLICANT: KAKANO, EILEEN
 APPLICANT: CLEMENTS, DAVID
 TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,195
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/488,807
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 TELECOMMUNICATION INFORMATION:
 REFERENCE DOCKET NUMBER: 4733-0003.20
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 VOLUME: 162

TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3381 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Dengue virus
 STRAIN: Serotype 2 (DEN-2)
 IMMEDIATE SOURCE:
 CLONE: Den-2 PR159/S1
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3381
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1216..1218
 OTHER INFORMATION: /note= "GAG(coding for Glu) is replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159"
 OTHER INFORMATION: strain(Citation #1)"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1258..1260
 OTHER INFORMATION: /note= "GTG(coding for Val) is replaced for GTT(coding for Val) for the wild-type DEN-2 PR159"
 OTHER INFORMATION: strain(Citation #1)"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1262..1264
 OTHER INFORMATION: /note= "ATT(coding for Ile) is replaced by GTC(coding for Val) for the wild-type DEN-2 PR159"
 OTHER INFORMATION: strain(Citation #1)"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1907..1929
 OTHER INFORMATION: /note= "AGT(Coding for Ser) is replaced by AGC(Coding for Ser) for the wild-type DEN-2 PR159"
 OTHER INFORMATION: strain(Citation #1)"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1
 OTHER INFORMATION: /note= "Start of coding strand sequence for Capsid"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 343
 OTHER INFORMATION: /note= "Start of coding strand sequence for preMembrane"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 616
 OTHER INFORMATION: /note= "Start of coding strand sequence for Membrane"
 OTHER INFORMATION: /note= "Start of coding strand sequence for Envelope"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 2326
 OTHER INFORMATION: /note= "Start of coding strand sequence for NS1"

PAGES: 167-180
DATE: 1988
US-08-937-195-2

Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

Qy 1 AATATGTTGAAACGGAGAAAACCGCG 28
Db 40 AATATGTTGAAACGGAGAAAACCGCG 67

RESULT 4
US-08-915-152-1
Sequence 1, Application US/08915152
Patent No. 6165477

GENERAL INFORMATION:
APPLICANT: IVI, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,152
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.21

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1

FEATURE:
NAME/KEY: misc_feature
LOCATION: Group 1(03, 1940, 1991, 2025)
OTHER INFORMATION: /note= "Positions in the S1 strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= [11]

NAME/KEY: misc_feature
LOCATION: 1218
OTHER INFORMATION: /note= "G is replaced by A for

OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1260
OTHER INFORMATION: /note= "T is replaced by G for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762
OTHER INFORMATION: /note= "G is replaced by A for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1929
OTHER INFORMATION: /note= "C is replaced by T for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2310
OTHER INFORMATION: /note= "A is replaced by N for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
sequence for Capsid."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
sequence for premembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
sequence for Membrane".
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
sequence for Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-915-152-1

Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAAAACCGCG 28
Db 40 AATATGCTGAAACGGAGAAAACCGCG 67

RESULT 5
US-08-915-152-2
Sequence 2, Application US/08915152
Patent No. 6165477
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
 CITY: WASHINGTON
 STATE: DC
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/915,152
 FILING DATE: 20-AUG-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/500,469
 FILING DATE: 10-JUL-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 28,959
 REFERENCE DOCKET NUMBER: 4733-0003.21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3381 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Dengue virus
 STRAIN: Serotype 2 (DEN-2)
 IMMEDIATE SOURCE:
 CLONE: Den-2 PR159/S1
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3381
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1216..1218
 OTHER INFORMATION: /note= "GAG(coding for Glu) is replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159 other information: strain(Citation #1)"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1258..1260
 OTHER INFORMATION: /note= "GTG(coding for Val) is replaced for GTR(coding for Val) for the wild-type DEN-2 PR159 other information: strain(Citation #1)"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1762..1764
 OTHER INFORMATION: /note= "ATT(coding for Ile) is replaced by AGT(coding for Ser) for the wild-type DEN-2 PR159 other information: strain(Citation #1)"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1927..1929
 OTHER INFORMATION: /note= "AGT(coding for Ser) is replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159 other information: strain(Citation #1)"
 OTHER INFORMATION: /citation= ([1])
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1

OTHER INFORMATION: /note= "Start of coding strand"
 OTHER INFORMATION: sequence for Capsid"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 343
 OTHER INFORMATION: /note= "Start of coding strand"
 OTHER INFORMATION: sequence for preMembrane"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 616
 OTHER INFORMATION: /note= "Start of coding strand"
 OTHER INFORMATION: sequence of Membrane"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 841
 OTHER INFORMATION: /note= "Start of coding strand"
 OTHER INFORMATION: sequence of Envelope"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 2326
 OTHER INFORMATION: /note= "Start of coding strand"
 OTHER INFORMATION: sequence for NS1"
 PUBLICATION INFORMATION:
 AUTHORS: Hahn, Y.S.
 JOURNAL: Virology
 VOLUME: 162
 PAGES: 167-180
 ;
 US-08-915-152-2
 Query Match 100.0%; Score 28; DB 3; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGAGAGAAACCCG 28
 Db 40 AATATGCTGAAACGGAGAGAAACCCG 67
 RESULT: 6
 US-09-376-463-2
 ; Sequence 2, Application US/09376463
 ; Patent No. 6749857
 ; GENERAL INFORMATION:
 ; APPLICANT: Hawaii Biotechnology Group, Inc.
 ; APPLICANT: Peters, Iain
 ; APPLICANT: Collier, Beth-Ann
 ; APPLICANT: McDonell, Michael
 ; APPLICANT: Ivy, John
 ; APPLICANT: Harada, Kent
 ; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
 ; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
 ; FILE REFERENCE: 24733-20005.20
 ; CURRENT APPLICATION NUMBER: US/09/376,463
 ; CURRENT FILING DATE: 2004-07-10
 ; PRIORITY APPLICATION NUMBER: US 08/904,227
 ; PRIORITY FILING DATE: 1997-07-31
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 3381
 ; TYPE: DNA
 ; ORGANISM: Dengue virus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3381)
 ;
 Query Match 100.0%; Score 28; DB 4; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGAGAGAAACCCG 28

```

Db 40 AATATGCTGAAACGCCAGAGAACCCGG 67
    NAME/KEY: misc_feature
    LOCATION: 616
    OTHER INFORMATION: /note= "Start of coding strand
    FEATURE:
        NAME/KEY: misc_feature
        LOCATION: 841
        OTHER INFORMATION: /note= "Start of coding strand
        OTHER INFORMATION: sequence for Membrane"
    FEATURE:
        NAME/KEY: misc_feature
        LOCATION: 2326
        OTHER INFORMATION: /note= "Start of coding strand
        OTHER INFORMATION: sequence for Envelope"
    FEATURE:
        NAME/KEY: misc_feature
        LOCATION: 2326
        OTHER INFORMATION: /note= "Start of coding strand
        PUBLICATION INFORMATION:
            AUTHORS: Hahn, Y.S.
            JOURNAL: Virology
            VOLUME: 162
            PAGES: 167-180
            DATE: 1988
        PCT-US96-07627-1
    Query Match 100.0%; Score 28; DB 5; Length 3381;
    Best Local Similarity 100.0%; Pred. No. 0.0012;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Qy 1 AATATGCTGAAACGCCAGAGAACCCGG 28
    Db 40 AATATGCTGAAACGCCAGAGAACCCGG 67

RESULT 7
PCT-US96-07627-1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
NUMBER OF SEQUENCES: 50
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07627
SEQUENCE CHARACTERISTICS:
SEQUENCE FOR SEQ ID NO: 1;
SEQUENCE ID: 1
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (ben-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: misc_feature
LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note= "Positions in the S1 strain
representing corrections to the wild type DEN-2 PR159 strain
reported by Hahn(Citation #1)" .
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1218
OTHER INFORMATION: /note= "G is replaced by A for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1260
OTHER INFORMATION: /note= "T is replaced by G for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762
OTHER INFORMATION: /note= "G is replaced by A for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1929
OTHER INFORMATION: /note= "C is replaced by T for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2310
OTHER INFORMATION: /note= "A is replaced by N for
Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
sequence for Capsid."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
sequence for premembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GAG(coding for Glu) is
replaced by GAA(coding for Val) for the wild-type DEN-2 PR15
OTHER INFORMATION: replaced for GAG(coding for Glu) for the wild-type DEN-2 PR15
OTHER INFORMATION: strain(Citation #1)" for the wild-type DEN-2 PR15
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
replaced by GAA(coding for Val) for the wild-type DEN-2 PR15
OTHER INFORMATION: replaced for GAG(coding for Glu) for the wild-type DEN-2 PR15
OTHER INFORMATION: strain(Citation #1)" for the wild-type DEN-2 PR15
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GAG(coding for Glu) is
replaced by GAA(coding for Val) for the wild-type DEN-2 PR15
OTHER INFORMATION: replaced for GAG(coding for Glu) for the wild-type DEN-2 PR15
OTHER INFORMATION: strain(Citation #1)" for the wild-type DEN-2 PR15
OTHER INFORMATION: /citation= ([1])

```

OTHER INFORMATION: /citation= ((1))

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: 1762..1764

OTHER INFORMATION: /note= "ATT(coding for Ile) is replaced by GTT(coding for Val) for the wild-type DEN-2 PR159"

OTHER INFORMATION: strain(citation #1)"

OTHER INFORMATION: /citation= ((1))

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: 1927..1929

OTHER INFORMATION: /note= "AGT(Coding for Ser) is replaced by AGC(Coding for Ser) for the wild-type DEN-2 PR159"

OTHER INFORMATION: strain(citation #1)"

OTHER INFORMATION: /citation= ((1))

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: 1

OTHER INFORMATION: /note= "Start of coding strand

OTHER INFORMATION: sequence for Capsid"

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: 343

OTHER INFORMATION: /note= "Start of coding strand

OTHER INFORMATION: sequence for preMembrane"

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: 616

OTHER INFORMATION: /note= "Start of coding strand

OTHER INFORMATION: sequence of Membrane"

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: 841

OTHER INFORMATION: /note= "Start of coding strand

OTHER INFORMATION: sequence of Envelope"

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: 2326

OTHER INFORMATION: /note= "Start of coding strand

OTHER INFORMATION: sequence for NS1"

PUBLICATION INFORMATION:

AUTHORS: Hahn, Y.S.

JOURNAL: Virology

VOLUME: 162

PAGES: 167-180

DATE: 1988

PCT-US96-17627-2

Query Match 100 %; Score 28; DB 5; Length 3381;

Best Local Similarity 100 %; Pred. No. 0.0012;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGGTAAACGCCAGAGAACCCG 28

Db 40 ATATGCTGAAACGCCAGAGAACCCG 67

RESULT 9

US-08-325-426B-1

Sequence 1, Application US/08325426B

Patent No. 607535

GENERAL INFORMATION:

APPLICANT: FU, Jianlin

APPLICANT: TAN, Boon-Hau

APPLICANT: YAP, Eu-Hian

APPLICANT: CHAN, Yow-Cheong

APPLICANT: TAN, Yin-Hwee

TITLE OF INVENTION: cDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON and VANDERHVE PC

STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

country: USA

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/325,426B

FILING DATE: 16-DEC-1994

INFORMATION FOR SEQ ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 10718 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA sequence corresponding to the genomic RNA of DEN1-S275/90

HYPOTHETICAL: NO

ANTI SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Dengue Fever Virus Type 1

STRAIN: S275/90

FEATURE:

NAME/KEY: CDS

LOCATION: 81..10268

US-08-325-426B-1

Query Match 94.3%; Score 26.4; DB 3; Length 10718;

Best Local Similarity 96.4%; Pred. No. 0.0055;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCCAGAGAACCCG 28

Db 120 ATATGCTGAAACGCCAGAGAACCCG 147

RESULT 10

US-09-270-767-9819/C

Sequence 9819, Application US/09270767

Patient No. 670341

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

FILE REFERENCE: File Reference: 7328-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9819

LENGTH: 1145

TYPE: DNA

ORGANISM: *Drosophila melanogaster*

US-09-270-767-9819

Query Match 66.4%; Score 18.6; DB 4; Length 1145;

Best Local Similarity 84.0%; Pred. No. 21;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCCAGAGAACCCG 26

Db 452 ATATGCTGAAACGCCAGAGAACCCG 428

RESULT 11

US-09-078-173A-11

Sequence 11, Application US/09078173A

Patient No. 6200754

GENERAL INFORMATION:

APPLICANT: Ian M. Whitehead

APPLICANT: Alan Slusarenko

APPLICANT: Duncan Gaskins
 APPLICANT: Alan Brash
 APPLICANT: Nathalie Tijet (PSIDIUM GUAYABA) 13-HYDROPEROXIDE
 TITLE OF INVENTION: LYASE AND USES THEREOF
 FILE REFERENCE: 06027.0001
 CURRENT APPLICATION NUMBER: US/09/078,173A
 CURRENT FILING DATE: 1998-05-13
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 11
 LENGTH: 1443
 TYPE: DNA
 ORGANISM: Capsicum annuum (green pepper)
 US-09-078-173A-11

Query Match 65.7%; Score 18.4; DB 3; Length 1443;
 Best Local Similarity 78.6%; Pred. No. 28;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGAGAGAAACCCCG 28
 Db 933 AAAATGCTGAGATGCAGAGAAACTGAG 960

RESULT 12 US-10-042-991-11
 Sequence 1.1, Application US/10042991
 Patent No. 6780621
 GENERAL INFORMATION:
 APPLICANT: Ian M. Whitehead
 APPLICANT: Alan Slusarenko
 APPLICANT: Duncan Gaskin
 APPLICANT: Alan Brash
 TITLE OF INVENTION: GUAVA (PSIDIUM GUAYABA) 13-HYDROPEROXIDE
 FILE REFERENCE: 06027.0001U3
 CURRENT APPLICATION NUMBER: US/10/042,991
 CURRENT FILING DATE: 2002-01-09
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 11
 LENGTH: 1443
 TYPE: DNA
 ORGANISM: Capsicum annuum (green pepper)
 US-10-042-991-11

Query Match 65.7%; Score 18.4; DB 4; Length 1443;
 Best Local Similarity 78.6%; Pred. No. 28;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGAGAGAAACCCCG 28
 Db 933 AAAATGCTGAGATGCAGAGAACTGAG 960

RESULT 13 US-08-224-391-52
 Sequence 52, Application US/08224391
 Patent No. 5744140
 GENERAL INFORMATION:
 APPLICANT: Paoletti, Enzo
 APPLICANT: Pincus, Steven E.
 TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 STREET: c/o William S. Frommer
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/224,391
 FILING DATE: 17-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2340
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4512 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-484-304-52

Query Match 65.7%; Score 18.4; DB 1; Length 4512;
 Best Local Similarity 78.6%; Pred. No. 35;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 US-08-811-566-5/C

Db 43 AATATGCTGAAACGCGAGAGAACCCGG 28

RESULT 15
 Sequence 5, Application US/08811566
 Patent No. 6127116

GENERAL INFORMATION:
 APPLICANT: Rice, Charles et al.
 TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
 TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/811,566
 FILING DATE: 03-MAR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1113-1-006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12980 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-811-566-5

Query Match 65.7%; Score 18.4; DB 3; Length 12980;
 Best Local Similarity 78.6%; Pred. No. 43;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 US-08-811-566-5

Db 9714 AATATGCTAATACGGCATACCCCG 9687

RESULT 17
 Sequence 5, Application US/09583110
 Patent No. 6699703

GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
 FILE REFERENCE: PATH0-07A
 CURRENT APPLICATION NUMBER: US/09/583,110
 CURRENT FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/107,433
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/085,131
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: US 60/051,553
 PRIOR FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 5322
 SEQ ID NO 2433
 LENGTH: 3351
 TYPE: DNA

RESULT 18
i ORGANISM: Streptococcus pneumoniae
us-09-583-110-2433
 Query Match 62.9%; Score 17.6; DB 4; Length 3351;
 Best Local Similarity 83.3%; Pred. No. 77;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGCCAGAGAAC 24
 Db 830 AATATGCTGAAACGCCAGAGAAC 853

RESULT 19
i Sequence 8086, Application US/09270767
i Patent No. 6703491
 GENERAL INFORMATION:
i APPLICANT: Homburger et al.
i TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
i FILE REFERENCE: File Reference: 7326-094
i CURRENT APPLICATION NUMBER: US/09/210,764
i CURRENT FILING DATE: 1999-03-17
i NUMBER OF SEQ ID NOS: 62517
i SOFTWARE: PatentIn Ver. 2.0
i SEQ ID NO 8086
i LENGTH: 763
i TYPE: DNA
i ORGANISM: Drosophila melanogaster
us-09-270-767-8086
 Query Match 62.1%; Score 17.4; DB 4; Length 763;
 Best Local Similarity 77.8%; Pred. No. 70;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGCCAGAGAACCC 27
 Db 534 AAAATCGAAAAACGCCAACAACCGC 560

RESULT 20
i Sequence 23368, Application US/09270767
i Patent No. 6703491
 GENERAL INFORMATION:
i APPLICANT: Homburger et al.
i TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
i FILE REFERENCE: File Reference: 7326-094
i CURRENT APPLICATION NUMBER: US/09/210,767
i CURRENT FILING DATE: 1999-03-17
i NUMBER OF SEQ ID NOS: 62517
i SOFTWARE: PatentIn Ver. 2.0
i LENGTH: 763
i TYPE: DNA
i ORGANISM: Drosophila melanogaster
us-09-270-767-23368
 Query Match 62.1%; Score 17.4; DB 4; Length 763;
 Best Local Similarity 77.8%; Pred. No. 70;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCCAGAGAAC 27
 Db 534 AAAATCGAAAAACGCCAACAACCGC 560

RESULT 21
i Sequence 1888/C
i Patent No. 6562958
 GENERAL INFORMATION:
i APPLICANT: Gary L. Breton et al.
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
i TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

Query Match 62.1%; Score 17.4; DB 3; Length 983;
 Best Local Similarity 77.8%; Pred. No. 74;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCCAGAGAACCGC 28
 Db 113 AGATCTGAACATCAATAAACCTCG 139

RESULT 22
i Sequence 1888, Application US/09328352
i Patent No. 6562958
 GENERAL INFORMATION:
i APPLICANT: Boesshore, Maury L.
i APPLICANT: McMaster, J. Russell

```

FILE REFERENCE: GT099-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO: 1888
LENGTH: 1227
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-1888

Query Match 62.1%; Score 17.4%; DB 4; Length 1227;
Best Local Similarity 77.8%; Pred. No. 77;
Matches 21; Conservative 0; Mismatches 6; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAACCGC 27
Db 964 AATATGAAAACGAAAGAAACCGC 938

RESULT 22
US-09-221-017B-558
Sequence 558 Application US/09221017B
Patent No. 644799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Discrete
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 1-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroe, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-94-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 558:
SEQUENCE CHARACTERISTICS:
LENGTH: 2646 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
;
```

```

; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 1...2846
; US-09-221-017B-558

Query Match 62.1%; Score 17.4%; DB 4; Length 2646;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 21; Conservative 0; Mismatches 6; Gaps 0;

Qy 2 ATATGTGAAACGGAGAACCGC 28
Db 1472 ACAGGATGAAAGCAAAGAATCCGC 1498

RESULT 23
US-09-549-872B-3
Sequence 3 Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaeert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9308670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 5026
TYPE: DNA
ORGANISM: Caenorhabditis elegans
; US-09-549-872B-3

Query Match 62.1%; Score 17.4%; DB 4; Length 5026;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Gaps 0;

Qy 10 AAACCGAGAGAACCGC 28
Db 2034 AAACCGAGAGAACCGC 2052

RESULT 24
US-09-549-872B-5
Sequence 5 Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaeert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9308670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 6612
TYPE: DNA
;
```

; ORGANISM: *Caenorhabditis elegans*
 Query Match Score 17.4%; DB 4; Length 6612;
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 10 AAACGCCAGAGAAACCGCG 28
 Db 2646 AAACGCCAGAGAAACCGCG 2664

RESULT 25
 US-09-549-872B-2
 ; Sequence 2, Application US/09549872B
 ; Patent No. 6540996
 ; GENERAL INFORMATION:
 ; APPLICANT: Zwaal, Richard
 ; APPLICANT: Groenin, Jose
 ; APPLICANT: Bogaert, Thierry
 ; TITLE OF INVENTION: COMPOUND SCREENING METHODS
 ; FILE REFERENCE: D00590/70008 (JRV/RE)
 ; CURRENT APPLICATION NUMBER: US/09/549, 872B
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: GB 9908670.4
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: GB 9912736.7
 ; PRIOR FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 11207
 ; TYPE: DNA
 ; ORGANISM: *Caenorhabditis elegans*
 us-09-549-872B-2

Query Match Score 17.4%; DB 4; Length 11207;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 10 AAACGCCAGAGAAACCGCG 28
 Db 2640 AAACGCCAGAGAAACCGCG 2658

RESULT 26
 US-08-611-107-32/c
 ; Sequence 32, Application US/08611107
 ; Patent No. 5801233
 ; GENERAL INFORMATION:
 ; APPLICANT: Haesekorn, Robert
 ; APPLICANT: Goricki, Piotr
 ; TITLE OF INVENTION: NUCLEAR ACID COMPOSITIONS ENCODING
 ; TITLE OF INVENTION: ACETYL-COA CARBOXYLASE AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/611-107
 ; FILING DATE: Concurrently Herewith

; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US SN 07/956,700
 ; FILING DATE: 02-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US PCT/US93/09340
 ; FILING DATE: 30-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US SN 08/422,560
 ; FILING DATE: 14-APR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kitchell, Barbara S.
 ; REGISTRATION NUMBER: 33,328
 ; REFERENCE/DOCKET NUMBER: ARCD-221
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 418-3000
 ; TELEFAX: (512) 474-7577
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3243 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-611-107-32

Query Match Score 17.2%; DB 1;
 Best Local Similarity 86.4%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 TATGTGAAACGCCAGAGAAC 24
 Db 926 TATGTGAAACGCCAGAGAAC 905

RESULT 27
 US-09-392-812A-1
 ; sequence 1, Application US/09392812A
 ; Patent No. 6537778
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Richard G.
 ; APPLICANT: Willingham, Aaron
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: A Eukaryotic Mechanosensory Transduction Channel
 ; FILE REFERENCE: 02407E-097600US
 ; CURRENT APPLICATION NUMBER: US/09/392, 812A
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 24358
 ; TYPE: DNA
 ; ORGANISM: *Drosophila melanogaster*
 ; FEATURE:
 ; OTHER INFORMATION: genomic nonpC (no-mechanoreceptor potential C)
 ; OTHER INFORMATION: nucleotide sequence
 ; US-09-392-812A-1

Query Match Score 17.2%; DB 4;
 Best Local Similarity 86.4%; Pred. No. 1.8e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 6 GCTGAAACGCCAGAGAACCGC 27
 Db 21468 GCAGAAAAGGACAGAAACCGC 21489

RESULT 28
 US-09-252-991A-116/c
 ; Sequence 116, Application US/09252991A
 ; Patent No. 6551705
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSBUDOMONAS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIORITY FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 1169
LENGTH: 435
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1169

Query Match Best Local Similarity 60.7%; Score 17; DB 4; Length 435;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ATGCTGAAACGGAGAAACCGCG 28
Db 425 AGTCGAAGCGCGAGAACCGCG 401

RESULT 29
Sequence 1, Application US/09/623034
Patent No. 6765128
GENERAL INFORMATION
APPLICANT: Klessig, Daniel F.
APPLICANT: Zhang, Shuguan
TITLE OF INVENTION: METHODS OF USING A PATHOGEN-ACTIVATABLE
FILE REFERENCE: RUT98-0073
CURRENT APPLICATION NUMBER: US/09/623,034
PRIORITY FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US99/03882
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1998-02-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 1725
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-623-034-1

Query Match Best Local Similarity 60.7%; Score 17; DB 4; Length 1725;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAAAC 25
Db 1231 AATATGCTTAACATAAGAATC 1255

RESULT 30
Sequence 12, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION
APPLICANT: Plasmid-derived type II
TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOSS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,159
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2355 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis subsp. cremoris
STRAIN: W39
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 744..1283
IDENTIFICATION METHOD: experimental
Other INFORMATION: /codon_start=744
Other INFORMATION: /product= "LladiI restriction endonuclease"
Other INFORMATION: /evidence= EXPERIMENTAL
Other INFORMATION: /Gene= "ORF"
Other INFORMATION: /number= 1
Other INFORMATION: /standard_name= "Gene coding for R.LladiII"
Other INFORMATION: /label= "R-LladiI"
Other INFORMATION: /note= "The first ten amino acids in this sequence may be doubtful. However, from base 773 this reading frame gives a homology with the Bsp6I endonuclease"
Other INFORMATION: /label= "Bsp6I"
Other INFORMATION: /note= "The sequence shows 60 % identity and 76 % similarity with the Bsp6I methylase."
FEATURE:
NAME/KEY: CDS
LOCATION: 1392..2342
IDENTIFICATION METHOD: experimental
Other INFORMATION: /codon_start= 1392
Other INFORMATION: /product= "LladiI methylase"
Other INFORMATION: /evidence= EXPERIMENTAL
Other INFORMATION: /Gene= "ORF"
Other INFORMATION: /number= 2
Other INFORMATION: /standard_name= "Gene coding for M.LladiII"
Other INFORMATION: /label= "M-LladiI"
Other INFORMATION: /note= "The sequence shows 60 % identity and 76 % similarity with the Bsp6I methylase."
US-08-913-159-12

Query Match Best Local Similarity 60.7%; Score 17; DB 3; Length 2355;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAAAC 25
Db 1326 AATATGTAAGGGAGATAAAC 1302

RESULT 31
Sequence 1251, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSBUDOMONAS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIORITY FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 1255
LENGTH: 2409

```

US-09-252-991A-11497/C
; Sequence 11497, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenstein et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11497
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11497

RESULT 32
; Sequence 4107, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4107
; LENGTH: 3378
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4107

Query Match 60.7%; Score 17; DB 4; Length 2409;
Best Local Similarity 80.0%; Pred No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4 ATGGCTAAACCGGAGAAACCGCG 28
Db 2208 AGGTCAAGCCGCGAGAAACCGCG 2184

RESULT 32
; Sequence 4107, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4107
; LENGTH: 3378
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4107

Query Match 60.7%; Score 17; DB 4; Length 3378;
Best Local Similarity 80.0%; Pred No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 TATGCCAAAACGGAGAAACCGC 27
Db 2791 TCTGCTGAAACCGAAGAGAAAGC 2815

RESULT 33
; Sequence 1156, Application US/0913294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalnudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SEQ ID NO 1156
; LENGTH: 287
; TYPE: DNA
; ORGANISM: zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550474H1
US-09-313-294A-1156

Query Match 60.0%; Score 16.8; DB 4; Length 287;
Best Local Similarity 75.0%; Pred No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 AATATGCTGAAACGGAGAGAAACCGCG 28
Db 59 ATTATGCTGAACTTCCGAGGAACGG 86

RESULT 34
; Sequence 11497, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 6977, Application US/09489039A
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6977
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6977

Query Match 60.0%; Score 16.8; DB 4; Length 1746;
Best Local Similarity 75.0%; Pred No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ATATGCTGAAACGGAGAGAAACCGCG 28
Db 745 ATTATGCTGACGGAGAGCCCTGCGCGC 772

RESULT 35
; Sequence 6977, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6977
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6977

Query Match 60.0%; Score 16.8; DB 4; Length 1746;
Best Local Similarity 75.0%; Pred No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ATATGCTGAAACGGAGAGAAACCGCG 28
Db 745 ATTATGCTGACGGAGAGCCCTGCGCGC 772

RESULT 36
; Sequence 1313-294A-522/C
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalnudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL program
; LENGTH: 287
; TYPE: DNA
; ORGANISM: zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550474H1
US-09-313-294A-522/C

Query Match 60.0%; Score 16.8; DB 4; Length 287;
Best Local Similarity 75.0%; Pred No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 AATATGCTGAAACGGAGAGAAACCGCG 28
Db 59 ATTATGCTGAACTTCCGAGGAACGG 86

```

SEQ ID NO 522
LENGTH: 297
TYPE: DNA
ORGANISM: Zea mays
FEATURE: misc feature
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID NO. 6476212 700549375H1
LOCATION: 23, 27, 63, 79, 95, 102, 122, 160, 197, 247, 261
OTHER INFORMATION: a, t, c, g, or other
US-09-313-29A-522

Query Match 59.3%; Score 16.6; DB 4; Length 297;
Best Local Similarity 82.6%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCTGAAACGCGAGAGAACCGCG 28
Db 55 GCTGAAACAGCAGGAGAACAGCG 33

RESULT 37
US-08-956-171E-314
Sequence 314, Application US/08956171E
Patent No. 653314
GENERAL INFORMATION:
APPLICANT: Charles Kunisch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 314:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-314

Query Match 59.3%; Score 16.6; DB 4; Length 702;
Best Local Similarity 82.6%; Pred. No. 1.6e-02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAAA 23
Db 521 AAGATGTTGAAACAGAGAGAA 543

RESULT 39
US-09-134-000C-295
Sequence 295, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIORITY APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1

Query Match 59.3%; Score 16.6; DB 4; Length 702;
Best Local Similarity 82.6%; Pred. No. 1.6e+02;

Query Match 59.3%; Score 16.6; DB 4; Length 314;
Best Local Similarity 82.6%; Pred. No. 1.6e+02;


```

; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO: 3544
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
;   US-09-270-767-3544

Query Match      59.3%;  Score 16.6.;  DB 3;  Length 10091;
Best Local Similarity 82.8%;  Pred. No. 2.8e+02;  Indels 0;  Gaps 0;
Matches 19;  Conservative 0;  Mismatches 4;  SEQ ID NO: 1
Qy   1 AATATGCTGAAACGGAGAGAA 23
Db   2890 AATATGTAAGTAGAGARA 2912

; RESULT 43
; US-09-270-767-8875/c
; Sequence 8875 Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO: 8875
;   LENGTH: 424
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
;   US-09-270-767-8875

Query Match      58.6%;  Score 16.4.;  DB 4;  Length 424;
Best Local Similarity 76.9%;  Pred. No. 1.8e+02;  Indels 6;  Gaps 0;
Matches 20;  Conservative 0;  Mismatches 6;  SEQ ID NO: 2
Qy   2 ATATGCTGAAACGGAGAGAAACCGC 27
Db   273 ATATGCTGAAATGCAAGGAAGCAGC 248

; RESULT 44
; US-09-270-767-24157/c
; Sequence 24157 Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO: 24157
;   LENGTH: 424
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
;   US-09-270-767-24157

Query Match      58.6%;  Score 16.4.;  DB 4;  Length 424;
Best Local Similarity 76.9%;  Pred. No. 1.8e+02;  Indels 6;  Gaps 0;
Matches 20;  Conservative 0;  Mismatches 6;  SEQ ID NO: 2
Qy   2 ATATGCTGAAACGGAGAGAAACCGC 27
Db   273 ATATGCTGAAATGCAAGGAAGCAGC 248

; RESULT 45
; US-09-270-767-3544/c
; Sequence 3544 Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/221,017B
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: FastSEQ for Windows Version 2.0b
;   SEQ ID NO: 3544
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
;   US-09-270-767-3544

Query Match      58.6%;  Score 16.4.;  DB 4;  Length 592;
Best Local Similarity 76.9%;  Pred. No. 1.9e+02;  Indels 0;  Gaps 0;
Matches 20;  Conservative 0;  Mismatches 6;  SEQ ID NO: 1
Qy   1 AATATGCTGAAACGGAGAGAAACCG 26
Db   436 ATTATGTTGAAACGAGGGAAAACG 411

; RESULT 46
; US-09-270-767-18826/c
; Sequence 18826 Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO: 18826
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
;   US-09-270-767-18826

Query Match      58.6%;  Score 16.4.;  DB 4;  Length 592;
Best Local Similarity 76.9%;  Pred. No. 1.9e+02;  Indels 0;  Gaps 0;
Matches 20;  Conservative 0;  Mismatches 6;  SEQ ID NO: 1
Qy   1 AATATGCTGAAACGGAGAGAAACCG 26
Db   436 ATTATGTTGAAACGAGGGAAAACG 411

; RESULT 47
; US-09-221-017B-105/c
; Sequence 105 Application US/09221017B
; Patent No. 644739
; GENERAL INFORMATION:
;   APPLICANT: Ross, Bruce C.
;   TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;   NUMBER OF SEQUENCES: 1120
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: MORRISON & FORESTER
;     STREET: 755 PAGE MILL ROAD
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
;   SOFTWARE: FastSEQ for Windows Version 2.0b
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/221,017B
;     FILING DATE: 23-DEC-1998
;     PATENT NO.: 6703491
;     APPLICATION NUMBER: US/09/221,017B
;     FILING DATE: 23-DEC-1998

```

```

CLASSIFICATION:
    / PRIOR APPLICATION DATA: PP1182
    / APPLICATION NUMBER: US-09-270-767-16913/C
    / FILING DATE: 31-DEC-1997
    / Sequence 16913, Application US/09270767
    / PRIOR APPLICATION DATA: PP1546
    / APPLICATION NUMBER: US-09-270-767-16913/C
    / FILING DATE: 30-JAN-1998
    / Sequence 16913, Application US/09270767
    / PRIOR APPLICATION DATA: PP2911
    / APPLICATION NUMBER: US-09-270-767-16913/C
    / FILING DATE: 09-APR-1998
    / Sequence 16913, Application US/09270767
    / PRIOR APPLICATION DATA: PCT/AU98/01023
    / APPLICATION NUMBER: US-09-270-767-16913/C
    / FILING DATE: 10-DEC-1998
    / Sequence 16913, Application US/09270767
    / ATTORNEY/AGENT INFORMATION:
        / NAME: Monroy, Gladys H
        / REGISTRATION NUMBER: 32, 430
        / REFERENCE/DOCKET NUMBER: 27340-20021.00
        / TELECOMMUNICATION INFORMATION:
            / TELEPHONE: 650-813-5600
            / TELEFAX: 650-94-0792
            / TELEX: 706141
    / SEQUENCE CHARACTERISTICS:
        / LENGTH: 652 base pairs
        / TYPE: nucleic acid
        / STRANDEDNESS: double
        / TOPOLOGY: circular
    / MOLECULE TYPE: DNA (genomic)
    / HYPOTHETICAL: NO
    / ANTI-SENSE: UNKNOWN
    / ORIGINAL SOURCE:
        / ORGANISM: PORPHYROMONAS GINGIVALIS
    / FEATURE:
        / NAME/KEY: misc_feature
    / LOCATION: 1...652
US-09-221-017B-105

RESULT 49
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 16913
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-16913

RESULT 50
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 16913
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-16913

RESULT 51
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 52
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 53
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 54
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 55
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 56
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 57
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 58
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 59
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

RESULT 60
    / Query Match      58 6%; Score 16.4; DB 4; Length 977;
    / Best Local Similarity 76.9%; Pred. No. 2.1e+02;
    / Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
    / FILE REFERENCE: File Reference: 7326-094
    / TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    / CURRENT APPLICATION NUMBER: US/09/270/767
    / CURRENT FILING DATE: 1999-03-17
    / NUMBER OF SEQ ID NOS: 62517
    / SOFTWARE: PatentIn Ver. 2.0
    / SEQ ID NO 1631
    / LENGTH: 977
    / TYPE: DNA
    / ORGANISM: Drosophila melanogaster
    / -US-09-270-767-1631

```

Qy 1 AATATGCTGAAACCGGAGAGAACCG 26
 ||| ||| ||| ||| ||| ||| |||
Db 1245 AATAGGCTAAAAATGAAAAGAACCG 1220

Search completed: January 19, 2005, 13:55:03
Job time : 52 secs

THIS PAGE BLANK (USPTO)

Result No.	Score	Query Match Length	DB ID	Description
1	28	100.0	28	Sequence 2, Appli
2	28	100.0	3381	Sequence 2, Appli
3	28	100.0	10724	Sequence 4, Appli
4	26.4	94.3	10735	Sequence 3, Appli
5	26	92.9	26	Sequence 23, Appli
6	26	92.9	14	Sequence 26, Appli
7	22	78.6	72	Sequence 108018,
8	19.6	70.0	594	Sequence 20593, A
c	9	67.9	765	Sequence 20594, A
c	10	19	67.9	Sequence 32952, A
c	11	18.8	67.1	Sequence 2266, Ap
c	12	18.6	1602	Sequence 2266, Ap

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 13:08:52 ; Search time 207 Seconds (without alignments)

777.222 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aataatgtgaaaacgcgagaaaaacgcg 28

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications NA:*

1: /cgn2_6/podata/1/pubna/us07_PUBCOMB.seq:*

2: /cgn2_6/podata/1/pubna/PCT_NEW_PUB.seq:*

3: /cgn2_6/podata/1/pubna/us06_NEW_PUB.seq:*

4: /cgn2_6/podata/1/pubna/us06_PUBCOMB.seq:*

5: /cgn2_6/podata/1/pubna/us07_NEW_PUB.seq:*

6: /cgn2_6/podata/1/pubna/PCTUS_PUBCOMB.seq:*

7: /cgn2_5/podata/1/pubna/us08_NEW_PUB.seq:*

8: /cgn2_6/podata/1/pubna/us08_PUBCOMB.seq:*

9: /cgn2_6/podata/1/pubna/us09A_PUBCOMB.seq:*

10: /cgn2_6/podata/1/pubna/us09C_PUBCOMB.seq:*

11: /cgn2_6/podata/1/pubna/us09_NEW_PUB.seq:*

12: /cgn2_6/podata/1/pubna/us10_PUBCOMB.seq:*

13: /cgn2_6/podata/1/pubna/us10_PUBCOMB.seq:*

14: /cgn2_6/podata/1/pubna/us10B_PUBCOMB.seq:*

15: /cgn2_6/podata/1/pubna/us10C_PUBCOMB.seq:*

16: /cgn2_6/podata/1/pubna/us10E_PUBCOMB.seq:*

17: /cgn2_6/podata/1/pubna/us10E_PUBCOMB.seq:*

18: /cgn2_6/podata/1/pubna/us10I_NEW_PUB.seq:*

19: /cgn2_6/podata/1/pubna/us11I_NEW_PUB.seq:*

20: /cgn2_6/podata/1/pubna/us60I_NEW_PUB.seq:*

21: /cgn2_6/podata/1/pubna/us60I_PUBCOMB.seq:*

RESULT 1

US-10-085-944-2

; Sequence 2, Application US/10085944

; Publication No. US20020155435A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Wei-Kung

; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS

; FILE REFERENCE: 12563-004001

; CURRENT APPLICATION NUMBER: US/10/085, 944

; CURRENT FILING DATE: 2002-06-18

; PRIOR APPLICATION NUMBER: 60/272, 535

; PRIOR FILING DATE: 2001-03-01

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 2

; LENGTH: 28

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

; US-10-085-944-2

Query Match Score 28; DB 13; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.0078;

Matches 28; Conservative 0; Mismatches 0;

Qy 1 AATATGCTGAAACGCCAGAGAGAACCGG 28

Db 1 AATATGCTGAAACGCCAGAGAGAACCGG 28

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 2
US-10-247-960-2

Sequence 2, Application US/10247960

Publication No. US20030175304A1

GENERAL INFORMATION:

APPLICANT: Hawaii Biotechnology Group, Inc.

APPLICANT: Peters, Tain

APPLICANT: Collier, Beth-Ann

APPLICANT: McDonald, Michael

APPLICANT: Ivy, John

APPLICANT: Harada, Kent

TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE

FILE REFERENCE: 24733-20005_01

CURRENT APPLICATION NUMBER: US/10/247,960

CURRENT FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: 09/376,463

PRIOR FILING DATE: 1999-08-18

PRIOR APPLICATION NUMBER: 08/904,227

PRIOR FILING DATE: 1997-07-31

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 2

LENGTH: 3381

TYPE: DNA

ORGANISM: Dengue virus

FEATURE:

NAME/KEY: CDS

LOCATION: (1) . . . (381)

US-10-247-960-2

Query Match

Best Local Similarity 100.0%

Pred. No. 0.014;

Length 3381;

Score 28;

DB 15;

Indels 0;

Gaps 0;

Matches 28;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Qy

1 AATATGCTGAAACGCCG 28

Db

4 AATATGGTAAACGCCG 67

RESULT 3
US-10-699-550-4

Sequence 4, Application US/10699550

Publication No. US20040197769A1

GENERAL INFORMATION:

APPLICANT: WONG, SUSAN J.

APPLICANT: SHI, PEI-YONG

TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS

FILE REFERENCE: 454311-2232.1

CURRENT APPLICATION NUMBER: US/10/699,550

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: 60/476,513

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: 60/422,755

PRIOR FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: 60/476,513

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: 60/422,755

PRIOR FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: PCT/US02/09036

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: 60/402,860

PRIOR FILING DATE: 2002-08-18

PRIOR APPLICATION NUMBER: 60/281,947

PRIOR FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/275,025

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO: 4

LENGTH: 10724

TYPE: DNA

ORGANISM: Dengue virus type 2

US-10-699-550-4

Query Match

100.0%

Score 28;

DB 18;

Length 10724;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCCG 28

Db 136 AATATGCTGAAACGCCG 163

RESULT 4
US-10-699-550-3

Sequence 3, Application US/10699550

Publication No. US20040197769A1

GENERAL INFORMATION:

APPLICANT: Wong, Susan J.

APPLICANT: Shi, Pei-Yong

TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS

FILE REFERENCE: 454311-2232.1

CURRENT APPLICATION NUMBER: US/10/699,550

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: 60/476,513

PRIOR FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: 60/422,755

PRIOR FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: 60/402,860

PRIOR FILING DATE: 2002-08-18

PRIOR APPLICATION NUMBER: 60/281,947

PRIOR FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/275,025

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: PatentIn Ver. 3.2

SEQ ID NO: 4

LENGTH: 10724

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

OTHER INFORMATION: Upper primer for Dengue virus type 2 detection

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCCG 28

Db 136 AATATGCTGAAACGCCG 163

RESULT 5
US-09-840-707A-23

Sequence 23, Application US/09840707A

Publication No. US2004007726A1

GENERAL INFORMATION:

APPLICANT: Freddieking, Terry M.

APPLICANT: Ignatyev, George M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS

TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS

FILE REFERENCE: 24881-301C

CURRENT APPLICATION NUMBER: US/09/840,707A

CURRENT FILING DATE: 2004-04-23

PRIOR APPLICATION NUMBER: 09/562,979

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/198,210

PRIOR FILING DATE: 1999-04-27

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO: 23

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

OTHER INFORMATION: Upper primer for Dengue virus type 2 detection

Db 325 ATACGCCGAAACGCCGAAACCCG 299

RESULT 10 US-10-363-345A-20594

; Sequence 32952, Application US/10363345A

; Publication No. US20040234960A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Method for determining the degree of methylation of defined cytosines in genomic DNA in the sequence context of 5'-CpG-3'

; CURRENT APPLICATION NUMBER: E01/1227

; CURRENT FILING DATE: 2003-03-03

; SEQ ID NO 20594

; LENGTH: 765

; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

; OTHER INFORMATION: CPG-island No: 20594

Query Match Score 19; DB 18; Length 765;

Best Local Similarity 81.5%; Pred. No. 1.3e+02; Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGGAAACGCCGAGAAACCCG 28

Db 441 ATACGCCGAAACGCCGAAACCCG 467

RESULT 11 US-10-369-493-32952/c

; Sequence 32952, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52032)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/3360,039

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 32952

; LENGTH: 1428

; TYPE: DNA

; ORGANISM: Xylella fastidiosa

; RESULT 12 US-10-369-493-32952

; Query Match Score 18.8; DB 15; Length 1428;

; Best Local Similarity 90.9%; Pred. No. 1.7e+02; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CTGAAACGCCGAGAAACCCG 28

Db 1184 CGGAAACGCCGAGAAACCCG 1163

; RESULT 12 US-10-156-761-2266

; Sequence 2266, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIIUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIORITY APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIORITY APPLICATION NUMBER: JP 2001-272697

; PRIORITY FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 2266

; LENGTH: 1602

; TYPE: DNA

; ORGANISM: Streptomyces avermitilis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1).-(1602)

; RESULT 13 US-10-156-761-1/c

; Sequence 1, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIIUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIORITY APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIORITY APPLICATION NUMBER: JP 2001-272697

; PRIORITY FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 1

; LENGTH: 9025608

; TYPE: DNA

; ORGANISM: Streptomyces avermitilis

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (418715)

; OTHER INFORMATION: a, t, c, g, other or unknown

; RESULT 14 US-10-156-761-1-1

; Query Match Score 18.6; DB 15; Length 1602;

; Best Local Similarity 84.0%; Pred. No. 2.1e+02; Matches 4; Indels 0; Gaps 0;

; RESULT 14 US-10-156-761-1

; Query Match Score 18.6; DB 15; Length 9025608;

; Best Local Similarity 84.0%; Pred. No. 3.9e+02; Matches 4; Indels 0; Gaps 0;

; RESULT 14 US-10-156-761-1

; Query Match Score 18.6; DB 15; Length 2778625

; Best Local Similarity 84.0%; Pred. No. 3.9e+02; Matches 4; Indels 0; Gaps 0;

RESULT 14
US-10-042-991-11
Sequence 11, Application US/10042991
Publication No. US2002142407A1
GENERAL INFORMATION:
APPLICANT: Ian M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Duncan Gaskin
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: GUAVA (PSIDIUM GUJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: LYASE AND USES THEREOF
FILE REFERENCE: 06027.0001U3
CURRENT APPLICATION NUMBER: US/10/042.91
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 1443
TYPE: DNA
ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match 65.7%; Score 18.4; DB 13; Length 1443;
Best Local Similarity 78.6%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAACCGCG 28
Db 933 AAAATGCTGAGATGCAAGAGAACTGTAG 960

RESULT 15
US-10-422-123A-2/C
Sequence 2, Application US/10422323A
Publication No. US20040214178A1
GENERAL INFORMATION:
APPLICANT: PFIZER, INC.
TITLE OF INVENTION: REPORTER-SELECTABLE HEPATITIS C VIRUS REPLICON
FILE REFERENCE: PC19102A (AG0190)
CURRENT APPLICATION NUMBER: US/10/422,323A
CURRENT FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: 60/375,667
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/375,667
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 12305
TYPE: DNA
ORGANISM: Unknown
FEATURE: UNKNOWN
OTHER INFORMATION: A cell line wherein the nucleic acid molecule is a self replicat
i OTHER INFORMATION: ng RNA molecule.
US-10-422-123A-2

Query Match 65.7%; Score 18.4; DB 18; Length 12305;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAACCGCG 28
Db 9039 AAATATGCTAAAAACGGGGATAACCCCGCG 9012

RESULT 16
US-10-422-323A-1/C
Sequence 1, Application US/10422323A
Publication No. US20040214178A1
GENERAL INFORMATION:
APPLICANT: PFIZER, INC.

; TITLE OF INVENTION: REPORTER-SELECTABLE HEPATITIS C VIRUS REPLICON
; FILE REFERENCE: PC19102A (AG0190)
; CURRENT APPLICATION NUMBER: US/10/422,323A
; Sequence 11, Application US/10042991
; CURRENT FILING DATE: 2002-04-24
; PRIORITY APPLICATION NUMBER: 60/375,667
; PRIORITY FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 12215
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A cell line wherein the nucleic acid molecule is a self replicat
; OTHER INFORMATION: ng RNA molecule.
; US-10-422-323A-1

Query Match 65.7%; Score 18.4; DB 18; Length 12315;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAACCGCG 28
Db 9209 AAATATGCTAAAAACGGGGATAACCCCGCG 9182

RESULT 17
US-09-238-076-5/C
Sequence 5, Application US/09238076
Patent No. US20030102540A1
GENERAL INFORMATION:
APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL S. HAVERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,076
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/034,756
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 6029-4831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
SEQUENCE CHARACTERISTICS:
LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-238-076-5

Query Match Similarity 65.7%; Score 18.4; DB 9; Length 12980;
 Best Local Similarity 78.6%; Pred. No. 3.4e+02; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 6; /

Qy 1 AATATGCTAACGGAGAGAAACCGCG 28
 Db 9714 AATATGCTAACGGAGAGAAACCGCG 9687

RESULT 18
 US-09-995-937-5/c
 / Sequence 5, Application US/0995937
 / Publication No. US20030028010A1
 / GENERAL INFORMATION:
 / APPLICANT: RICE, CHARLES et al.
 / TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
 / VIRUS (HCV) AND USES THEREOF
 / NUMBER OF SEQUENCES: 21
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: HOWELL & HAERKAMP, L.C.
 / STREET: 7733 FORSYTH BLVD., SUITE 1400
 / CITY: ST. LOUIS
 / STATE: MO
 / ZIP: USA
 / ZIP: 63105

COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/995,937
 / FILING DATE: 28-Nov. US20030028010A1-2001
 / CLASSIFICATION: <Unknown>
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US/09/034,756
 / FILING DATE: 04-May-1998
 / ATTORNEY/AGENT INFORMATION:
 / NAME: HOLLAND, DONALD R.
 / REGISTRATION NUMBER: 35,197
 / REFERENCE/DOCKET NUMBER: 6029-4831
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 314-727-5188
 / TELEFAX: 314-727-6092
 / INFORMATION FOR SEQ ID NO: 5:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 12980 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / MOLECULE TYPE: CDNA
 / HYPOTHETICAL: NO
 / ANTI-SENSE: NO
 / SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-995-937-5

Query Match Similarity 65.7%; Score 18.4; DB 10; Length 12980;
 Best Local Similarity 78.6%; Pred. No. 3.4e+02; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 6; /

Qy 1 AATATGCTAACGGAGAGAAACCGCG 28
 Db 9714 AATATGCTAACGGAGAGAAACCGCG 9687

RESULT 19
 US-09-918-995-27460
 / Sequence 5, Application US/09918953
 / Publication No. US20030073623A1
 / GENERAL INFORMATION:
 / APPLICANT: HYSEQ, Inc.
 / TITLE OF INVENTION: NOVEL NUCLEAR ACID SEQUENCES OBTAINED
 / FROM VARIOUS CDNA LIBRARIES
 / FILE REFERENCE: 20411-756
 / CURRENT APPLICATION NUMBER: US/09/918,995
 / CURRENT FILING DATE: 2001-07-30
 / PRIOR APPLICATION NUMBER: US/09/235,076
 / PRIOR FILING DATE: 1999-01-20
 / NUMBER OF SEQ ID NOS: 38054
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 27460
 / LENGTH: 452
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (1)...(452)
 / OTHER INFORMATION: n = A,T,C or G

US-09-918-995-27460

Query Match Score 65.0%; Best Local Similarity 87.0%; Pred. No. 2.8e+02; Length 452; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0; SEQ ID NO: US-09-823-245A-434

RESULT 21

Qy 1 AATATGCTGAAACGGAGAGAA 23
Db 172 AAGATGCTGAAACAGGAGAGAA 194

GENERAL INFORMATION:

APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, KamaLakar
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

FILE REFERENCE: GIN 6401

CURRENT APPLICATION NUMBER: US/09/823.245A

PRIOR APPLICATION NUMBER: 2001-03-29

PRIOR FILING DATE: 6/194,941

NUMBER OF SEQ ID NOS: 631

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 434

LENGTH: 2179

TYPE: DNA

ORGANISM: Homo sapiens

US-09-823-245A-434

Query Match Score 65.0%; Best Local Similarity 87.0%; Pred. No. 3.4e+02; Length 2179; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0; SEQ ID NO: US-09-764-891-7878/C

RESULT 22

Qy 1 AATATGCTGAAACGGAGAGAA 23
Db 1550 AAGATGCTGAAACAGGAGAGAA 1572

GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PCT006

CURRENT APPLICATION NUMBER: US/09/764.891

CURRENT FILING DATE: 2001-01-17

Pilot application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 10231

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 9875

TYPE: DNA

ORGANISM: Homo sapiens

US-09-764-891-7878

Query Match Score 65.0%; Best Local Similarity 87.0%; Pred. No. 4e+02; Length 9875; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0; SEQ ID NO: 7978

RESULT 23

Qy 1 AATATGCTGAAACGGAGAGAA 23
Db 636 AAGATGCTGAAACAGGAGAGAA 614

GENERAL INFORMATION:

APPLICANT: Zhou, Yongwei
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21/153223/B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO: 130933

LENGTH: 529

TYPE: DNA

ORGANISM: Glycine max

FEATURE: NAME/KEY: unsure

LOCATION: (1)-(529)

OTHER INFORMATION: unsure at all n locations

FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_8923C.1

US-10-424,599-130933

Query Match Score 62.9%; Best Local Similarity 83.3%; Pred. No. 5.3e+02; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0; SEQ ID NO: 4 ATGCTTAAACCGGAGAAACCGC 27

Qy 135 ATGAAACCAACCGGAGAAACCGC 158

Db 135 ATGAAACCAACCGGAGAAACCGC 158

RESULT 24

Qy 4 ATGCTTAAACCGGAGAAACCGC 27
Db 135 ATGAAACCAACCGGAGAAACCGC 158

GENERAL INFORMATION:

APPLICANT: Wang, Youzhen
APPLICANT: Steimann, Kathleen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14034

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 11819

LENGTH: 550

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: misc_feature

LOCATION: 506,-549, 550

OTHER INFORMATION: n = A,T,C or G

US-10-198-846-11819

Query Match Score 62.9%; Best Local Similarity 83.3%; Pred. No. 5.3e+02; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0; SEQ ID NO: 1 ATATGCTGAAACGGAGAGAAC 24

Qy 1 ||||| ||||| ||||| ||||| |||||

Db 1 ||||| ||||| ||||| ||||| |||||

Db 45 AATTGGAAACTGGAGAAC 22

RESULT 25
 US-10-198-846-3468/C
 ; Sequence 3468, Application US/10198846
 ; GENERAL INFORMATION:
 ; APPLICANT: Steimann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
 ; FILE REFERENCE: MRI-019
 CURRENT APPLICATION NUMBER: US/10/198,846
 CURRENT FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/306,220
 PRIOR FILING DATE: 2001-07-18
 NUMBER OF SEQ ID NOS: 14084
 SEQ ID NO: 3468
 LENGTH: 838
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 557, 616, 641, 691, 749, 765, 796, 798, 815, 821
 OTHER INFORMATION: n = A, T, C or G

US-10-198-846-3468

Query Match 62.9%; Score 17.6; DB 14; Length 838;
 Best Local Similarity 83.3%; Pred. No. 5.6e+4; Indels 0; Gaps 0;

Qy 1 AATATGTTAACGCGAGAAC 24
 Db 108 AATTTGGAAACTGGAGAAC 85

RESULT 26
 US-10-398-221-2508
 ; Sequence 2508, Application US/10398221
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNST, Frederik
 ; APPLICANT: GLASER, Philippe

TITLE OF INVENTION: Listeria innocua, genome and applications

FILE REFERENCE: 344 702 - US
 CURRENT APPLICATION NUMBER: US/10/398,221
 CURRENT FILING DATE: 2003-03-27
 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 PRIOR FILING DATE: 2001-10-04
 NUMBER OF SEQ ID NOS: 4025
 SEQ ID NO: 2508
 LENGTH: 945
 TYPE: DNA
 ORGANISM: Listeria innocua

Query Match 62.9%; Score 17.6; DB 16; Length 945;
 Best Local Similarity 83.3%; Pred. No. 5.7e+02; Indels 0; Gaps 0;

Qy 3 TATGCTGAACCGGAGAAC 26
 Db 193 TATGCTGAAACATGAGAACAG 216

Query Match 62.9%; Score 17.6; DB 16; Length 945;
 Best Local Similarity 83.3%; Pred. No. 5.7e+02; Indels 0; Gaps 0;

Qy 193 TATGCTGAAACATGAGAACAG 216

RESULT 27
 US-10-398-221-2571
 ; Sequence 2571, Application US/10398221
 ; General Information:
 ; Publication No. US20040018514A1

APPLICANT: KUNST, Frederik
 APPLICANT: GLASER, Philippe
 TITLE OF INVENTION: Listeria innocua, genome and applications
 FILE REFERENCE: 344 702 - US
 CURRENT APPLICATION NUMBER: PCT/FR 01/03 061
 CURRENT FILING DATE: 2003-03-27
 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 PRIOR FILING DATE: 2001-10-04
 NUMBER OF SEQ ID NOS: 4025
 SEQ ID NO: 2571
 LENGTH: 945
 TYPE: DNA
 ORGANISM: Listeria innocua

US-10-398-221-2571

Query Match 62.9%; Score 17.6; DB 16; Length 945;
 Best Local Similarity 83.3%; Pred. No. 5.7e+02; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TATGCTGAACCGGAGAAC 26
 Db 193 TATGCTGAAACATGAGAACAG 216

RESULT 28
 US-10-398-221-553
 ; Sequence 553, Application US/10398221
 ; General Information:
 ; Publication No. US20040018514A1

APPLICANT: KUNST, Frederik
 APPLICANT: GLASER, Philippe
 TITLE OF INVENTION: Listeria innocua, genome and applications
 FILE REFERENCE: 344 702 - US
 CURRENT APPLICATION NUMBER: US/10/398,221
 CURRENT FILING DATE: 2003-03-27
 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 PRIOR FILING DATE: 2001-10-04
 NUMBER OF SEQ ID NOS: 4025
 SEQ ID NO: 553
 LENGTH: 966
 TYPE: DNA
 ORGANISM: Listeria innocua

US-10-398-221-553

Query Match 62.9%; Score 17.6; DB 16; Length 966;
 Best Local Similarity 83.3%; Pred. No. 5.7e+02; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TATGCTGAACCGGAGAAC 26
 Db 214 TATGCTGAAACATGAGAACAG 237

RESULT 29
 US-10-398-221-554
 ; Sequence 554, Application US/10398221
 ; Publication No. US20040018514A1
 ; General Information:
 ; APPLICANT: KUNST, Frederik
 ; APPLICANT: GLASER, Philippe
 ; TITLE OF INVENTION: Listeria innocua, genome and applications
 ; FILE REFERENCE: 344 702 - US

FILE REFERENCE: 344 702 - US

CURRENT APPLICATION NUMBER: US/10/398,221
 CURRENT FILING DATE: 2003-03-27
 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 PRIOR FILING DATE: 2001-10-14
 PRIOR APPLICATION NUMBER: FR 00/12 697
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 4025
 SOFTWARE: PatentIn version 3.0

SEQ ID NO 554
 LENGTH: 966
 TYPE: DNA
 ORGANISM: Listeria innocua

US-10-398-221-554

Query Match 62.9%; Score 17.6; DB 16; Length 1646;
 Best Local Similarity 83.3%; Pred. No. 6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TGCTGAAACCGGAGAGAAACCGCG 28
 Db 210 TGAAAGAACGGCGAAAACCGCG 187

RESULT 31
 US-08-3119-974A-1/c
 ; Sequence 1, Application US/08319974A
 ; Publication No. US2003104576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nvice, Jonathan W.
 ; TITLE OF INVENTION: Attenuated Viruses and Method of Making
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kenneth D. Sibley
 ; STREET: Post Office Box 34009
 ; CITY: Charlotte
 ; STATE: No. US2003104576A1th Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/319,974A
 ; FILING DATE: 07-OCT-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sibley, Kenneth D.
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5218-27
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-881-3140
 ; TELEFAX: 919-881-3175
 ; TELEX: 575102
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9718 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA

US-10-282-122A-29374/c
 ; Sequence 29374, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangau
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA_034A
 ; CURRENT FILING DATE: US/10/282,122A
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-16
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR FILING DATE: 2001-02-09
 ; Remaining Prior Application Number: 60/269,308
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 29374
 ; LENGTH: 1646
 ; TYPE: DNA
 ; ORGANISM: Neisseria meningitidis

US-10-282-122A-29374
 ; Sequence 1, Application US/10398221
 ; Publication No. US20040018514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNST, Frederik
 ; APPLICANT: GLASER, Philippe
 ; TITLE OF INVENTION: Listeria innocua, genome and applications
 ; FILE REFERENCE: 344 702 - US
 ; CURRENT APPLICATION NUMBER: US/10/398,221
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 ; PRIOR FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: FR 00/12 697
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 4025
 SOFTWARE: PatentIn version 3.0

SEQ ID NO: 9
 LENGTH: 684707
 TYPE: DNA
 ORGANISM: Listeria innocua
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(end)
 OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
 US-10-398-221-9

Query Match Score 62.9%; Pred. No. 1.2e+03; Length 684707;
 Best Local Similarity 83.3%; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TATGCTGAAGCGGAGAAACCG 26
 Db 660685 TATGCTGAACATGAAACAG 660708

RESULT 33
 US-10-398-221-9/c
 Publication No. US20040018514A1
 Sequence 9, Application US/10398221
 GENERAL INFORMATION:
 APPLICANT: KUNST, Frederik
 ATTORNEY: GLASER, Philippe
 TITLE OF INVENTION: Listeria innocua, genome and applications
 FILE REFERENCE: 344 702 - US
 CURRENT APPLICATION NUMBER: US/10/398,221
 CURRENT FILING DATE: 2003-03-27
 PCT/FR 01/03 061
 PRIOR FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: FR 00/12 697
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 4025
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 9
 LENGTH: 684707
 TYPE: DNA
 ORGANISM: Listeria innocua
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(end)
 OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
 US-10-398-221-9

Query Match Score 62.9%; Pred. No. 1.2e+03; Length 684707;
 Best Local Similarity 83.3%; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TATGCTGAACCGGAGAAACCG 26
 Db 182545 TATGCTGAACATGAAACAG 182522

RESULT 34
 US-10-398-221-2058/c
 Sequence 2058, Application US/10398221
 Publication No. US20040018514A1
 GENERAL INFORMATION:
 APPLICANT: KUNST, Frederik
 ATTORNEY: GLASER, Philippe
 TITLE OF INVENTION: Listeria innocua, genome and applications
 FILE REFERENCE: 344 702 - US
 CURRENT APPLICATION NUMBER: US/10/398,221
 CURRENT FILING DATE: 2003-03-27
 PCT/FR 01/03 061
 PRIOR FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: FR 00/12 697

PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 4025
 SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2058
 LENGTH: 3011208
 TYPE: DNA
 ORGANISM: Listeria innocua
 US-10-398-221-2058

Query Match Score 62.9%; Pred. No. 1e+03; Length 3011208;
 Best Local Similarity 83.3%; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TATGCTGAACAGCGAGAAACCG 26
 Db 2434485 TATGCTGAACATGAAACAG 2434462

RESULT 35
 US-10-767-701-19049/c
 Publication No. US20040172684A1
 Sequence 15049, Application US/10767701
 GENERAL INFORMATION:
 APPLICANT: Kovacic, David K.
 ATTORNEY: Zhou, Yihua
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
 FILE REFERENCE: 38-21(535)B
 CURRENT APPLICATION NUMBER: US/10/767,701
 CURRENT FILING DATE: 2004-01-29
 NUMBER OF SEQ ID NOS: 63128
 SEQ ID NO: 19049
 LENGTH: 341
 TYPE: DNA
 ORGANISM: Sorghum bicolor
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3480-019-P1-K1-F12
 US-10-767-701-19049

Query Match Score 62.1%; Pred. No. 6.2e+02; Length 341;
 Best Local Similarity 77.8%; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTAACCGGAGAAACCGC 27
 Db 335 AAANGGTAAAACGGAGAAACCGC 309

RESULT 36
 US-09-738-269-20/c
 Sequence 20, Application US/09738269
 Publication No. US20030185848A1
 GENERAL INFORMATION:
 APPLICANT: JOHNSTON, STEPHEN A.
 ATTORNEY: STEINKE-HALE, KATHERINE
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING CHLAMYDIA PSITTACI
 FILE REFERENCE: UTS/659
 CURRENT APPLICATION NUMBER: US/09/738,269
 CURRENT FILING DATE: 2000-12-18
 NUMBER OF SEQ ID NOS: 61
 SEQ ID NO: 20
 LENGTH: 379
 TYPE: DNA
 ORGANISM: Chlamydia psittaci
 US-09-738-269-20

Query Match Score 62.1%; Pred. No. 1.2e+03; Length 379;

Best Local Similarity 77.8%; Pred. No. 6.2e+02; Mismatches 0; Indels 6; Gaps 0; Best Local Similarity 77.8%; Pred. No. 6.2e+02; Mismatches 0; Indels 6; Gaps 0;

Qy 2 ATATGCTGAAACGGCAGAGAACCGG 28 Qy 1 ATATGCTGAAACGGCAGAGAACCGG 27
Db 59 ATATGCTGATAATAGGAGAACCTGG 33 Db 79 ATATGCTGAAAGGGGACAAAAACAC 105

RESULT 37 US-10-023-437-20/C
Sequence 20, Application US/10023437
GENERAL INFORMATION:
APPLICANT: JOHNSTON, STEPHEN A.
APPLICANT: STEMKIE-HALE, KATHERINE
APPLICANT: SYKES, KATHRYN F.
APPLICANT: KALTENBOECK, BERNHARD
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
FILE REFERENCE: UTSD-736US
CURRENT APPLICATION NUMBER: US/10/023,437
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 379
TYPE: DNA
ORGANISM: Chlamydia psittaci

Query Match 62.1%; Score 17.4; DB 13; Length 379;
Best Local Similarity 77.8%; Pred. No. 6.2e+02; Mismatches 0; Indels 6; Gaps 0; Best Local Similarity 77.8%; Pred. No. 6.2e+02; Mismatches 0; Indels 6; Gaps 0;

Qy 2 ATATGCTGAAACGGCAGAGAACCGG 28 Qy 2 ATATGCTGAAACGGCAGAGAACCGG 28
Db 59 ATATGCTGATAATAGGAGAACCTGG 33 Db 294 ATATCCAAAACGCGAGGGCACCG 268

RESULT 39 US-10-424-599-53946/c
Sequence 53946, Application US/10424599
Publication No. US2004031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
Title of Invention: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 53946
LENGTH: 528
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_19726C.1

Query Match 62.1%; Score 17.4; DB 16; Length 528;
Best Local Similarity 77.8%; Pred. No. 6.5e+02; Mismatches 0; Indels 6; Gaps 0;

US-10-424-599-53946

RESULT 40 US-10-027-632-237136/c
Sequence 237136, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827-129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-01-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-07-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 237136
LENGTH: 558
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature

Query Match 62.1%; Score 17.4; DB 17; Length 382;

RESULT 38 US-10-437-963-17200
Sequence 17200, Application US/10437963
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yinhua
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
Title of Invention: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 17200
LENGTH: 382
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(382)
OTHER INFORMATION: unsure at all n locations

US-10-437-963-17200
OTHER INFORMATION: Clone ID: PAT_MRT4530_22877C.1
FEATURE:
NAME/KEY: misc_feature

```

;
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-237136/C

Query Match Score 17.4; DB 13; Length 558;
Best Local Similarity 62.1%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 6;
Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGGATAAACCGC 27
Db 263 AATATGGTGAAGAGGGATATAACCGC 237

RESULT 41
US-10-027-632-237136/C
Sequence 237136, Application US/10027632
Publication No. US20030204075A9

GENERAL INFORMATION
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 10887.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 237136
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-237136/C

Query Match Score 17.4; DB 15; Length 558;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 6;
Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGGATAAACCGC 27
Db 263 AATATGGTGAAGAGGGATATAACCGC 237

RESULT 42
US-10-363-345A-34197/C
Sequence 34197, Application US/10363345A
Publication No. US20040234960A1

GENERAL INFORMATION
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 34198
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 34197

Qy 2 ATATGCTGAAACGGAGGATAAACCGC 28
Db 166 ATACCGCAAACGGAAAAACCGG 140

RESULT 43
US-10-363-345A-34198
Sequence 34198, Application US/10363345A
Publication No. US20040234960A1

GENERAL INFORMATION
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 34198
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 34198

Qy 2 ATATGCTGAAACGGAGGATAAACCGC 28
Db 166 ATACCGCAAACGGAAAAACCGG 140

RESULT 44
US-10-363-345A-38631/C
Sequence 38631, Application US/10363345A
Publication No. US20040234960A1

GENERAL INFORMATION
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 38631
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 38631

Qy 2 ATATGCTGAAACGGAGGATAAACCGC 28
Db 424 ATACCGCAAACGGAAAAACCGG 450

RESULT 45
US-10-363-345A-38631/C
Sequence 38631, Application US/10363345A
Publication No. US20040234960A1

GENERAL INFORMATION
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 38631
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 38631

Qy 2 ATATGCTGAAACGGAGGATAAACCGC 28
Db 424 ATACCGCAAACGGAAAAACCGG 450

```

Query Match 62.1%; Score 17.4%; DB 18; Length 691;
 Best Local Similarity 77.8%; Pred. No. 6.7e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 6;

Qy 2 ATATGCTGAAACGCGAGAGAACCGGG 28
 Db 226 ATAAACCGAAAACCTGAAAAAACCGGG 200

RESULT 45
 US-10-363-345A-38632 Application US/103633345A
 Sequence 38632, Application US/103633345A
 Publication No. US20040234960A1
 GENERAL INFORMATION:
 APPLICANT: Alexander Olek
 ATTORNEY: Christian Piepenbrock
 APPLICANT: Kurt Berlin
 TITLE OF INVENTION: Method for determining the degree of methylation of defined
 FILE REFERENCE: E01/1227
 CURRENT APPLICATION NUMBER: US/10/363-345A
 CURRENT FILING DATE: 2003-03-03
 NUMBER OF SEQ ID NOS: 40712
 SEQ ID NO 38632
 LENGTH: 691
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 OTHER INFORMATION: CpG-island No: 38632
 US-10-363-345A-38632

Query Match 62.1%; Score 17.4%; DB 18; Length 691;
 Best Local Similarity 77.8%; Pred. No. 6.7e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 6;

Qy 2 ATATGCTGAAACGCGAGAGAACCGGG 28
 Db 466 ATAAACCGAAAACCTGAAAAAACCGGG 492

RESULT 47
 US-10-282-122A-36749/c
 Sequence 36749, Application US/10282122A
 Publication No. US2004029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 ATTORNEY: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 ATTORNEY: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 ATTORNEY: Zyskind, Judith
 APPLICANT: Wall, Daniel
 ATTORNEY: Trawick, John
 APPLICANT: Carr, Grant
 ATTORNEY: Yamamoto, Robert
 APPLICANT: Forayth, R.
 ATTORNEY: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIORITY APPLICATION NUMBER: 60/191,078
 PRIORITY FILING DATE: 2003-03-21
 PRIORITY APPLICATION NUMBER: 60/205,848
 PRIORITY FILING DATE: 2000-05-23
 PRIORITY APPLICATION NUMBER: 60/207,727
 PRIORITY FILING DATE: 2000-05-26
 PRIORITY APPLICATION NUMBER: 60/230,335
 PRIORITY FILING DATE: 2000-05-06
 PRIORITY APPLICATION NUMBER: 60/230,347
 PRIORITY FILING DATE: 2000-09-09
 PRIORITY APPLICATION NUMBER: 60/242,578
 PRIORITY FILING DATE: 2000-10-23
 PRIORITY APPLICATION NUMBER: 60/253,625
 PRIORITY FILING DATE: 2000-11-27
 PRIORITY APPLICATION NUMBER: 60/257,931
 PRIORITY FILING DATE: 2000-12-22
 PRIORITY APPLICATION NUMBER: 60/267,636
 PRIORITY FILING DATE: 2001-01-09
 PRIORITY APPLICATION NUMBER: 60/269,308
 Remaining Prior Application data removed - See File Wrapper or PAM.
 NUMBER OF SEQ ID NOS: 78634
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 36749
 LENGTH: 774

```

; TYPE: DNA
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-36749

Query Match 62.1%; Score 17.4; DB 16; Length 778;
Best Local Similarity 77.8%; Pred. No. 6.8e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 21; Conservative 0; Number of SEQ ID NOS: 61
; CURRENT APPLICATION NUMBER: US/09/738,269
; FILE REFERENCE: UTSD-1659
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; NUMBER OF SEQ ID NOS: 61
; PRIORITY FILING DATE: 2000-12-18
; SEQ ID NO: 22
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22

RESULT 48
US-10-011-013-11

; GENERAL INFORMATION:
; APPLICANT: Beshore, Maury L
; McMaster, J Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey Minamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
ZIP: 60619
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,033
; FILING DATE: 13-JUN-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; JOURNAL: J. Gen. Virol.
; VOLUME: 70
; PAGES: 1065-1073
; DATE: 1989
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-011-013-11

Query Match 62.1%; Score 17.4; DB 13; Length 2520;
Best Local Similarity 77.8%; Pred. No. 7.8e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 21; Conservative 0; Number of SEQ ID NOS: 61
; CURRENT APPLICATION NUMBER: US/09/738,269
; FILE REFERENCE: UTSD-1659
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; NUMBER OF SEQ ID NOS: 61
; PRIORITY FILING DATE: 2000-12-18
; SEQ ID NO: 22
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22

RESULT 50
US-10-023-437-22/C
Sequence 22, Application US/10023437
; Publication No. US20030183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEINKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOCK, BERNARD
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID SEQUENCES OF CHLAMYDIA
; CURRENT APPLICATION NUMBER: US/10/023,437
; FILE REFERENCE: UTSD-736JS
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; SEQ ID NO: 69
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-10-023-437-22

Query Match 62.1%; Score 17.4; DB 13; Length 2520;
Best Local Similarity 77.8%; Pred. No. 7.8e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 21; Conservative 0; Number of SEQ ID NOS: 61
; CURRENT APPLICATION NUMBER: US/09/738,269
; FILE REFERENCE: UTSD-1659
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; NUMBER OF SEQ ID NOS: 61
; PRIORITY FILING DATE: 2000-12-18
; SEQ ID NO: 22
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22

Query Match 62.1%; Score 17.4; DB 13; Length 2520;
Best Local Similarity 77.8%; Pred. No. 7.8e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 21; Conservative 0; Number of SEQ ID NOS: 61
; CURRENT APPLICATION NUMBER: US/09/738,269
; FILE REFERENCE: UTSD-1659
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; NUMBER OF SEQ ID NOS: 61
; PRIORITY FILING DATE: 2000-12-18
; SEQ ID NO: 22
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22

Query Match 62.1%; Score 17.4; DB 13; Length 2520;
Best Local Similarity 77.8%; Pred. No. 7.8e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 21; Conservative 0; Number of SEQ ID NOS: 61
; CURRENT APPLICATION NUMBER: US/09/738,269
; FILE REFERENCE: UTSD-1659
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; NUMBER OF SEQ ID NOS: 61
; PRIORITY FILING DATE: 2000-12-18
; SEQ ID NO: 22
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22

```

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 12:51:42 ; Search time 1550 Seconds

 568.266 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aataatgtgaaaacgcgagagaaaaaccggcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3282875 seqs, 18219865308 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 50 summaries

Database : EST:*

```

1: 9b_est1:*
2: 9b_est2:*
3: 9b_hnc:*
4: 9b_est3:*
5: 9b_est4:*
6: 9b_est5:*
7: 9b_est6:*
8: 9b_gss1:*
9: 9b_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	20.6	73.6	776	7 CP996467	CF996467 AGENCOURT
c 2	19.8	70.7	720	7 CP455745	CP455745 AGENCOURT
c 3	19.6	70.0	301	6 CB078143	hj63104.g
c 4	19.6	70.0	712	7 CF372439	CF372439 CSECS052D
c 5	19.6	70.0	722	7 CF512147	CF512147 Cabud0003
c 6	19.4	69.6	734	7 CF512236	Cabud0003
c 7	19.4	69.3	464	2 BE841207	BE841207 QV4-SH002
c 8	19	67.9	520	9 CR305770	CR305770 Medicago
c 9	19	67.9	559	9 TA262BHQ1Q	TA262BHQ1Q
c 10	19	67.9	568	8 AQ945632	AQ945692 Sheared D
c 11	19	67.9	576	9 TA140D12P	AL466434 T. brucei
c 12	19	67.9	580	2 BB776235	BB776235 MY-12-F-0
c 13	19	67.9	602	1 AL673619	AL673619 AL673619
c 14	19	67.9	629	1 AL647632	AL647632 AL647632
c 15	19	67.9	633	6 CA349616	CA349616 620082 NC
c 16	19	67.9	649	6 CA356841	CA356841 629106 NC
c 17	19	67.9	738	9 AG363192	AG363192 Mus muscu
c 18	19	67.9	768	9 CC50335	CC50335 CH240_344
c 19	19	67.9	870	9 AG186531	AG186531 Pan trogl
c 20	19	67.9	988	7 CP995511	CP995511 AGENCOURT
c 21	18.8	67.1	1687	2 BF128456	BF128456 60181042
c 22	18.6	66.4	407	6 CP198531	CP198531 EST026 T
c 23	18.6	66.4	456	4 BG659286	BG659286 TGES02ya2
c 24	18.6	66.4	563	7 CF939381	CF939381 NCESTqabs

ALIGNMENTS

RESULT 1
CP996467/c

LOCUS CP996467 mRNA Linear EST 25-NOV-2003

DEFINITION AGENCOURT_16394292 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7037741

5', mRNA Sequence.

CP996467

ACCESSION CP996467.1

VERSION GI:38517318

KEYWORDS EST;

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE NIH-MGCG http://mgc.ncbi.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL National Cancer Institute / NIH

COMMENT Contact: Daniela S. Gesthard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Len Zon, Harvard

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:

http://image.liln.gov

Plate: LILAM14788 row: e column: 03

High quality sequence stop: 734.

Location/Qualifiers

FEATURES Source

1. .776

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7055"

/clone="IMAGE:7037741"

/tissue="whole body"

/lab_host="DB10B"

/clone_id="NIH_ZGC_7"

/note="Vector: pEXPRESS1; Site1: NotI; Site2: EcoRV;

Bulk tissue was collected from a whole adult individual

from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRI sites of pExpress-1. Library was size-selected for >1 kb fragments and normalized. A non-normalized version of this library is also available (NIH ZGC 10). Library was constructed by Open Biosystems (Huntsville, AL).

RESULT 3 CB078143	ORGANISM	Hedotis terminalis
	DEFINITION	CB078143_91 Hedotis terminalis flower - Stage 2 (NYBG) Hedotis terminalis cDNA clone hJ63h04, mRNA sequence.
	ACCESSION	CB078143
	VERSION	CB078143.1 GI:27891580
	KEYWORDS	
	SOURCE	
	ORGANISM	Hedotis terminalis
	DEFINITION	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; asterids; Lamiales; Gentianales; Rubiales; Rubioideae; Spermacaece; Hedotis.
	ACCESSION	1 (bases 1 to 301)
	REFERENCE	Levesque,M.P., Triggg,R.W., Motley,T., Karari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Bajji,V., Martenssen,R.A., McCombie,R.W., Benfey,P. and Stevenson,D.
RESULT 2 CF155745	TITLE	Expressed tag sequences from Hedotis terminalis flower - Stage 2 (NYBG)
	JOURNAL	Unpublished (2003)
	COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mccombie@csbl.org Plate: mccombie@csbl.org Row: h column: 04
	FEATURES	Seq primer: -2IM13UnivRev High quality sequence stop: 301. Location/Qualifiers 1. . 301
	source	/organism="Hedotis terminalis" /mol_type="mRNA" /db_xref="taxon:219667" /clone="hJ63h04" /dev_stage="pre-embryo" /clone_lib="Hedotis terminalis flower - Stage 2 (NYBG)" /note="Organ: Flower; Vector: pBR-CMV; Site: XbaI; Xhol" Site 2: Eco RI; Date: Completed 12/18/01. Submitted to CSHL-12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii; NYBG herbarium voucher "TM2562"
	ORIGIN	Query Match 70 0%; Score 19.6; DB 6; Length 301; Best Local Similarity 84.6%; Pred. No. 3.7e+02; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0
	FEATURES	Qy 3 TATGGAAACGGAGAGAACCGG 28 Db 212 TATGGCTGAAACGTGACAGAGCGGGC 237
	source	
	ORGANISM	
	DEFINITION	
RESULT 4 CF372439	LOCUS	CF372439_712 bp mRNA linear EST 27-AUG-2000
	DEFINITION	CSECS02D08_FLOn0012 CabSau Normalised Flower Stage 12 (PL0n0012)
	ACCESSION	Vitis vinifera cDNA clone CSECS02D08_3', mRNA sequence.
	VERSION	CF372439.1 GI:34319685
	KEYWORDS	
	SOURCE	
	ORGANISM	Vitis vinifera
	DEFINITION	Vitis vinifera Spermatophyta; Magnoliophyta; eudicots; asterids; Vitaceae; Vitis.
	ACCESSION	1 (bases 1 to 712)
	REFERENCE	Looco,P., Davies,C. and Thomas,M.R.
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 3 CB078143	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	DEFINITION	
	ACCESSION	
	REFERENCE	
RESULT 2 CF155745	ORGANISM	
	DEFINITION	
	ACCESSION	
	VERSION	

Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon	
JOURNAL	Unpublished (2003)
COMMENT	Contact: Mark R. Thomas CSIRO Plant Industry PO Box 350, Glen Osmond, SA, 5064, Australia Tel: 61 8 83038600 Fax: 61 8 83038601 Email: Mark.R.Thomas@csiro.au Seq primer: CCCAGTCACGCGTCAAAACG (M13 Forward) PolyA+ Yes
FEATURES	Location/Qualifiers
Source	1. .712 /organism="Vitis vinifera" /mol_type="mRNA" /cultivar="Cabernet Sauvignon" /db_xref="taxon:29760" /clone_id="CBSICSU52D08" /sex="Hermaphrodite" /dev_stage="12 - modified B-L system" /clone_lib="CabSau Normalised Flower Stage 12 (FLONLINE)" /note="Organ: Inflorescence including flowers; Vector: PZL; Normalised cDNA library from immature inflorescences at stage 12 of the modified B-L system. Tissue coll: from field grown plants. A description of the modified system can be found in the paper by B. G. Coombes 'A system of a system for identifying grapevine growth stages (1995) Aust. J. Grape and Wine Res. 1: 104-110."
ORIGIN	Query Match 70.0%; Score 19.6; DB 7; Length 712; Best Local Similarity 84.6%; Pred. No. 3.9e+02; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	1 ANTATGCTGAANCCGAGAACCCG 26
Ddb	374 ATTATGCTGAACCTCGAAAGAACTG 399
RESULT 5	
LOCUS	CP512147 722 bp mRNA linear EST 09-SI
DEFINITION	CABUD0003_1F A10 Vitis vinifera cv. cabernet sauvignon (Clone Bud - CABUD Vitis vinifera cDNA Clone CABUD0003_1F_A10 S , mm sequence.
ACCESSION	CP512147
VERSION	CP512147.1
KEYWORDS	GI:34543915
SOURCE	Vitis vinifera
ORGANISM	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheobionts; Magnoliophyta; Magnoliidae; eudicotyledons; core eudicots; Rosids; Vitaceae; Vitis.
REFERENCE	1 (bases 1 to 722)
AUTHORS	Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Jones,K. and Cook,D.
TITLE	Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
JOURNAL	Unpublished (2003)
COMMENT	Contact: Douglas Cook, PhD CAES Genome Facility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drcook@ucdavis.edu
FEATURES	Location/Qualifiers
Source	1. .722 /organism="Vitis vinifera" /mol_type="mRNA" /cultivar="Cabernet Sauvignon (Clone 8)"

'Cabernet Sauvignon' Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-Veraison. Samples vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in conjunction as follows:

5'-AAGCTGTGGATTCATGCCAGATGGCCATTACGCCGGG-3' and
5'-ATTCTAGGGCGGAGGGGCCACATG-DT(30)NN-3'. Library was constructed using the Clonetech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

low stringency conditions."

RESULT 8	
CR305770	520 bp DNA linear Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago truncatula, genomic survey sequence.
LOCUS	CR305770
DEFINITION	Medicago truncatula (barrel medic)
ACCESSION	CR305770.1
VERSION	GI:44851914
KEYWORDS	GSS.
SOURCE	Medicago truncatula (barrel medic)
ORGANISM	Medicago truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
REFERENCE	1 (bases 1 to 520)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (25-FEB-2004) Genoscope - Centre National de Séquençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
FEATURES	- Web : www.genoscope.cns.fr
source	1. 520 /organism="Medicago truncatula" /mol_type="genomic DNA" /cultivar="Jemalong A17" /db_xref="taxon:380" /clone_id="MTE1" /note="Vector: PlindigoBAC ; Site_1: EcoRI ; Site_2: EcoRI ; Debelle F. and Chalhoub B.-Genoscope sequence ID : mtel-25N13RM1"
ORIGIN	Query Match 67.9%; Score 19; DB 9; Length 520; Best Local Similarity 81.5%; Prod. No. 7.1e+02; Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
REFERENCE	RESULT 9
AUTHORS	TA262H01Q
DEFINITION	T. brucei sheared genomic DNA clone 262h01, reverse sequence.
ACCESSION	AL487728
VERSION	GI:118850764
KEYWORDS	GSS.
SOURCE	Trypanosoma brucei
ORGANISM	Trypanosoma brucei Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE	1 (bases 1 to 559)
AUTHORS	Hall N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk and hinxton,
FEATURES	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.p?l1=et2=QV4-SN0024-200 seq=300-3-a07&t3=2000-07-20&t4=1) Seq primer: puc 18 forward High quality sequence start: 10 High quality sequence stop: 248. Location/Qualifiers
source	1..464 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_id="SN0024" /note="Organ: stomach_normal; Vector: puc18; Site_1: SmAI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 106,716 - Ludwig Institute for Cancer Research profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplicons were performed under

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD.

FEATURES source

1. .559 /Location/Qualifiers

1. .559 /organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="262h01"

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 559;
Best Local Similarity 81.5%; Pred. No. 7.1e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
Db 454 ATATGGAGAAAACGGAGCAAGGACG 480

RESULT 10 A0945692/c

LOCUS A0945692 568 bp DNA linear GSS 27-JAN-2000

DEFINITION Sheared DNA-49G5. T/F Sheared DNA Trypanosoma brucei genomic clone

ACCESSION A0945692

VERSION A0945692.1

KEYWORDS GI:6768880

SOURCE GSS.

ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 568)

AUTHORS El-Sayed,N., Zhao,S., Gill,H., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Uliu,E., Melville,S., Doneelson,J., Fraser,C. and Adams,M.

TITLE Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library

JOURNAL Unpublished (1999)

COMMENT Other GSSs: Sheared DNA-49G5.TF
Contact: Majib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org

Clabs: shotgun

Location/Qualifiers

1. 568 /organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927/4 GUTat 10.1"

/db_xref="taxon:5691"

/clone="Sheared DNA-49G5"

/clone.lib="Sheared DNA"

/note="Vector: pUC18; Site_1: SmaI; Constructed at The DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tmdb/tbdb/."

FEATURES source

1. 568 /Location/Qualifiers

1. 568 /organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927/4 GUTat 10.1"

/db_xref="taxon:5691"

/clone.lib="Sheared DNA"

/note="Vector: pUC18; Site_1: SmaI; Constructed at The DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tmdb/tbdb/."

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 576;
Best Local Similarity 81.5%; Pred. No. 7.1e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
Db 231 ATATGGAGAAAACGGAGCAAGGACG 257

RESULT 12

BE776235	BE776235	590 bp mRNA linear	EST 20-SEP-2000	This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.			
LOCUS	MY-12-F-04	PinfesteransBY Phytophthora infestans cDNA, mRNA sequence.		cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.			
DEFINITION	MY-12-F-04			Vector: pCS107; Site_1: EcoRI; Site_2: NotI			
ACCESSION	BE776235			Host: Escherichia coli DH10B			
VERSION	BE776235.1			Sanger Xenopus tropicalis EST project 2001			
KEYWORDS	EST			TROPICALIS SEQUENCE ID: TNeu062m06_pkSP6			
SOURCE				Sequencing primer: SP6.			
ORGANISM				Location/Qualifiers			
				/organism="Xenopus tropicalis"			
REFERENCE				/mol_type="mRNA"			
AUTHORS	Ramoun,S., Haber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.			/db_xref="taxon:8364"			
TITLE	Initial assessment of gene diversity for the oomycete pathogen			/dev_stage="neurula"			
JOURNAL	Phytophthora infestans based on expressed sequences			/lab_host="Escherichia coli DH10B"			
MEDLINE	Fungal Genet. Biol. 28 (2), 94-106 (1999)			/clone_lib="XGC-neurula"			
PUBMED	10587472			/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; CDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."			
COMMENT	Contact: Govers F.			/db_xref="taxon:8364"			
Laboratory of Phytopathology				/clones="TNeu062m06"			
Wageningen University				/dev_stage="neurula"			
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands				/lab_host="Escherichia coli DH10B"			
Tel: 31 317 483 138				/clone_lib="XGC-neurula"			
Fax: 31 317 483 412				/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; CDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."			
Email: Francine.Govers@medew.fyto.wau.nl.				/db_xref="taxon:8364"			
FEATURES				/clones="TNeu062m06"			
source				/dev_stage="neurula"			
				/lab_host="Escherichia coli DH10B"			
				/clone_lib="XGC-neurula"			
				/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; Total RNA was isolated from mycelium of <i>P. infestans</i> DDR1602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycelial) and the successive number of the microtiter plate (e.g. MY-06-A-04)."			
ORIGIN				/db_xref="taxon:8364"			
				/clones="TNeu062m06"			
				/dev_stage="neurula"			
				/lab_host="Escherichia coli DH10B"			
				/clone_lib="XGC-neurula"			
				/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; Total RNA was isolated from mycelium of <i>P. infestans</i> DDR1602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycelial) and the successive number of the microtiter plate (e.g. MY-06-A-04)."			
RESULT	14			/db_xref="taxon:8364"			
LOCUS	AL647632	629 bp mRNA	linear	EST 20-NOV-2003			
DEFINITION				AL647632 XGC-gastrula Xenopus tropicalis cDNA clone TGas037f09 5'			
QY	2	ATATGCTGAAACGGAGAAACCGCG 28		mRNA sequence.			
Db	202	ATATGCTGAAACGGAGAAACCGCG 228		EST.			
ORIGIN				Xenopus tropicalis (western clawed frog)			
				ORGANISM			
				Xenopus tropicalis			
				Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
				Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			
				Xenopodinae; Xenopus; Silurana.			
				1 (bases 1 to 629)			
REFERENCE	Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.			Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.			
AUTHORS				Unpublished (2003)			
TITLE				On Dec 13, 2001 this sequence version replaced gi:17655342.			
JOURNAL				COMMENT			
				Contact: Huckle E.			
				Sanger Institute			
				Hinxton, Cambridgeshire, CB10 1SA, UK			
				Email: trop@sanger.ac.uk			
				This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.			
				cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.			
				Vector: pCS107; Site_1: EcoRI; Site_2: NotI			
				Host: Escherichia coli XL1-blue			
				Sanger Xenopus tropicalis EST Project 2001			
				TROPICALIS SEQUENCE ID: TGas037f09_pkSP6			
				Sequencing primer: SP6.			
FEATURES				Location/Qualifiers			
source				/organism="Xenopus tropicalis"			
				/mol_type="mRNA"			
				/db_xref="taxon:8364"			
				/clone="TGas037f09"			
				/dev_stage="gastrula" (stages 10.5-12 mixed)"			
RESULT	13			/dev_stage="gastrula" (stages 10.5-12 mixed)"			
LOCUS	AL673619	602 bp mRNA	linear	EST 10-NOV-2003			
DEFINITION				AL673619 mRNA sequence.			
ACCESSION				EST.			
VERSION				Xenopus tropicalis (western clawed frog)			
SOURCE				Xenopus tropicalis			
ORGANISM				Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
				Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			
				Xenopodinae; Xenopus; Silurana.			
REFERENCE	Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.			Xenopus tropicalis EST Project 2001			
AUTHORS				Unpublished (2003)			
TITLE				On Mar 18, 2002 this sequence version replaced gi:19529975.			
JOURNAL				COMMENT			
				Contact: Taylor R.			
				Sanger Institute			
				Hinxton, Cambridgeshire, CB10 1SA, UK			
				Email: trop@sanger.ac.uk			

/lab host="Escherichia coli XL1-blue"
 /clone lib="Xgc-gastrula"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
ORIGIN

Query Match 67.9%; Score 19; DB 1; Length 629;
 Best Local Similarity 81.5%; Pred. No. 7.2e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 ATATGCTGAAACGGAGAGAACCGGG 28
Db 234 ATAGCTGAAACGGAGAGAACCGGG 260

RESULT CA349616
LOCUS CA349616 633 bp mRNA linear EST 05-NOV-2002
DEFINITION NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT142M04_C_G02
5',mRNA sequence.
VERSION CA349616
VERSION CA349616.1 GI:24594787
KEYWORDS
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleosteii;
 Protocanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G., Koop, B., Gahr, S.A., Palti, Y., and Quackenbush, J.
AUTHORS
TITLE Sequence analysis of a rainbow trout cDNA library and creation of a gene index
JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
COMMENT Contact: Rexroad CB
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross_match v0.990329.
FEATURES
Source
Location/Qualifiers
 1..649
 /organism="Oncorhynchus mykiss"
 /mol type="mRNA"
 /db_xref="taxon:8022"
 /tissue type="pooled"
 /lab host="DH10B"
 /clone lib="NCCCWA 1RT"
 /note="Vector: pcMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
ORIGIN

Query Match 67.9%; Score 19; DB 6; Length 649;
 Best Local Similarity 81.5%; Pred. No. 7.2e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 AATATGCTGAAACGGAGAGAACCGGC 27
Db 469 AATATCGAGACTGGAGAGAGCTGC 495

RESULT AG363192/c
LOCUS AG363192
DEFINITION Mus musculus molossinus 738 bp DNA linear GSS 03-JUN-2004
5',mRNA sequence.
VERSION AG363192.1 GI:4794397
KEYWORDS
SOURCE Mus musculus molossinus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Hattori M., Toyoda, A., Noguchi, H., Kojima, T., and Sakaki, Y.
AUTHORS
JOURNAL Unpublished
TITLE BAC end Sequences of Library MSNG01
REFERENCE 2 (bases 1 to 738)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T., and Sakaki, Y.
JOURNAL Direct Submission
TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0015, Japan
 (E-mail: hattori@gsb.riken.jp; URL: http://hgp.gsc.riken.go.jp/;
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)

RESULT 16
LOCUS CA356841 CA356841 649 bp mRNA linear EST 05-NOV-2002

COMMENT	Clones are derived from the mouse BAC library MSMg01. For BAC library availability, Please contact Kunuya Abe (abe@rci.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1, Toyodai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rci.riken.jp		FEATURES	source	Seq primer: T7 Class: BAC ends Location/Qualifiers
PRIMERS					1. 1. 768 /organism="Bos taurus" /mol_type="genomic DNA" /strain="breed: Hereford" /db_xref="taxon:9913" /clone="CH240_344G2" /sex="Male" /cell_type="Blood" /clone_1ib="CHORI-240" /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull Li Domino 98375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
SEQUENCING	: TJ				
VECTOR	: pBACE3.6				
R.SITE 1	: EcorI				
R.SITE 2	: EcoRI.	Location/Qualifiers			
	1. .738				
ORGANISM	/organism="Mus musculus molossinus"				
	/mol_type="genomic DNA"				
	/sub_species="molossinus"				
	/db_xref="taxon:57486"				
	/clone="MSMg01-164N14.TJ"				
	/sex="male"				
	/tissue_Type="mixture of kidney and spleen"				
	/clone_Lib="MSMg01 Mouse Male BAC Library"				
ORIGIN					
Query Match	67.9%	Score 19;	DB 9;	Length 738;	RESULT 1.9
Best Local Similarity	81.5%;	Pred. No. 7.3e-02;			AGI.86531/C
Matches	22;	Conservative	0;	Mismatches 5; Indels 0; Gaps 0;	LOCUS
Qy	1 AATATGCTAAACGGAGGAAACCGC 27				Pan troglodytes DNA, clone: RP43-060P05.TJ, genomic survey sequence.
Db	690 AATATACCGAAAAGCGAGGGAAAGCGC 664				ACCESSION AGI.86531
					VERSION GI:16716211
KEYWORDS	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.				
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.				
TITLE	BAC and sequences of Library RPCI-43				
JOURNAL	Unpublished				
REPERE	2 (bases 1 to 870)				
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22, Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbees@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-03-9111, Fax:81-45-03-9170)				
COMMENT	Clones are derived from the Chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.				
PRIMERS					
SEQUENCING	Sequencing: TJ				
JOURNAL	The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6				
COMMENT	Contact: Rob Holt				
REFERENCE	Holt, R., Stott, J., Yang, G., Barber, S., Shnailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., We, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., McWilliam, S., Barris, W., Dalrymple, B.-P. and Tellam, R.				
AUTHORS					
KEYWORDS					
SOURCE					
ORGANISM	Bos taurus (cow)				
REFERENCE	Other GSss: CH240_344G2.TARBAC1.3P2				
AUTHORS					
KEYWORDS					
SOURCE					
COMMENT	Unpublished (2003)				
COMMENT	Contact: Rob Holt				
SEQUENCING	Sequencing: TJ				
JOURNAL	The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6				
COMMENT	Email: rholt@bcgpc.ca				
REFERENCE	Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejorg@mail.cho.org).				
AUTHORS					
KEYWORDS					
SOURCE					
COMMENT	Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering-information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.				
COMMENT	Plate: 344 row: G column: 2				
FEATURES	source	Seq primer: T7 Class: BAC ends Location/Qualifiers			
REFERENCE	1. .870 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" /clone="RP43-060P05.TJ" /sex="male" /cell_type="lymphocytes" /clone_1ib="RPCI-43 Chimpanzee Male BAC Library"				
AUTHORS					
KEYWORDS					
SOURCE					
COMMENT	Query Match 67.9%; Score 19; DB 9; Length 870;				

Best Local Similarity 81.5%; Pred. No. 7.3e+02; Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Score 19; DB 7; Length 988; Qy 1 AATATGCTGAACGGAGAAGAACCGC 28 Db 690 ATATGCCAAATCGCGAGCACGGCC 664

RESULT 20
CF995511/c
LOCUS CF995511 988 bp mRNA linear EST 25-NOV-2003
DEFINITION AGENCOURT 16028690 NIH MGC_217 Homo sapiens cDNA clone IMAGE:30524078 5', mRNA sequence.
ACCESSION CF995511
VERSION CF995511.1
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgc.ncbi.nih.gov/.
AUTHORS Unpublished (1999)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10407 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Arrayed by: M. Bento Soares, University of Iowa
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDAM603 row: a column: 15
High quality sequence stop: 407.

FEATURES Source
Location/Qualifiers 1..98
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524078"
/tissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 217"
/note="Vector: PYX-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned;
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into PYX-AsC vector. Average insert size
0.5-1Kb. Adaptors 5' (AATTGCGACGAGC)3', and 5'd
(CCCTCGTGCGCG)3'. 3' Linker sequence - GCGCCCCCTGAGAGCC T18.
Sequencing primers 3', end: T3 promoter primer 5'd
(ATPAACCCCTCACTAAAGCCA)3'; 5' End: T7 promoter primer 5'd
(TAATACGACTCACTATAGCC)3'; Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."

ORIGIN Query Match 67.9%; Score 19; DB 7; Length 988;
Best Local Similarity 81.5%; Pred. No. 7.4e+02; Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Score 27; DB 727 ATTATGCCAAACGAGAAGAACCGC 701

RESULT 21
BF128456 LOCUS BF128456 1687 bp mRNA linear EST 24-OCT-2000
DEFINITION mRNA sequence.
ACCESSION BF128456
VERSION BF128456.1 GI:10367496
KEYWORDS SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1687)
AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.llnl.gov
Plate: LiCM891 row: c column: 12
High quality sequence start: 26
High quality sequence stop: 165.
FEATURES Source
Location/Qualifiers 1..1687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone="IMAGE:14031059"
/note="Organ: uterus; Vector: pCR2.1-TOPO; Site 1: XbaI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XbaI sites using the following 5' adapter:
GGCAAGAGG). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN Query Match 67.1%; Score 18.8; DB 2; Length 1687;
Best Local Similarity 90.9%; Pred. No. 9.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 CTGAAACGCGAGAGAACCGCG 28
Db 694 CAGACAGCGAGAGAACCGCG 715

RESULT 22
CF198531/c LOCUS CF198531 407 bp mRNA linear EST 01-AUG-2003
DEFINITION Tamarix androssowii sequence.
ACCESSION CP198531
VERSION EST
KEYWORDS SOURCE Tamarix androssowii
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllaceae; Tamariaceae; Tamarix.
REFERENCE 1 (bases 1 to 407)
AUTHORS Wang, Y.; Yang, C.; Jiang, J.; Liu, G.; Wu, J. and Liu, Z.
TITLE EST acquired from cDNA library of Tamarix androssowii treated with

NaHCO3	Unpublished (2003)	The primary library was mass excised as phagemids and rescued in SO1R cells. The plasmid library was recovered from the SO1R cells and transformed in mass into DH10B (Genetog, Research Genetics, Inc.) for sequencing. WARNING: This library may contain a small percentage contaminants from human fibroblast cells."
JOURNAL	Contact: Yucheng Wang	
COMMENT	Forestry Source and Environment College	
Northeast Forestry University	Hexing 26, Harbin, Heilongjiang, 150040, P.R. China	
Tel: 086-451-2190607	Email: WANGYUCHENG1029@YAHOO.COM.CN.	
FEATURES	Source	
ORIGIN	Location/Qualifiers	
	1. .407 /organism="Tamarix androssowii" /mol_type="mRNA" /db_xref="taxon:189785" /tissue_type="leaf" /clone_lib="Tamarix androssowii leaf"	
ORIGIN	Query Match	Score 18.6; DB 4; Length 456;
	Best Local Similarity 84.0%; Pred. No. 1.1e+03	Score 18.6; DB 4; Length 456;
	Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Score 18.6; DB 4; Length 456;
RESULT 24	LOCUS	CF939381/c
	DEFINITION	NCESTGab57905.y1
		563 bp mRNA, linear
		CDNA Library 2 Neospora caninum
		CDNA 5' similar to SWYC27_HUMAN HYPOTHETICAL PROTEIN
		CGI-27.; mRNA sequence.
Qy	ACCESSION	CF939381
	VERSION	CF939381.1
	KEYWORDS	GI:38438622
Db	SOURCE	EST.
	ORGANISM	Neospora caninum
		Neospora caninum
		Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimerida;
		Sarcocystidae; Neospora.
	REFERENCE	1 (bases 1 to 563)
	AUTHORS	Cole,R., Rogarty,S., Tang,K., Howe,D.K., Sibley,L.D., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wyllie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J.J., Ronko,I.I., Tsagareishvili,R., Fedele,M., Belaygorod,L., Franklin,C., Carr,L.M., Grow,A., Maguire,L., Wadkins,J., Ritchey,J., Waterston,R., and Wilson,R.
	TITLE	USDA-WashU Neospora EST Project
	JOURNAL	Unpublished (2000)
	COMMENT	Contact: Sandy Clifton, Ph.D. ~ Neospora
		USDA-WashU Neospora EST Project
		Washington University School of Medicine
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
		Tel: 314 286 1800
		Fax: 314 286 1810
		Email: estwats@wustl.edu
		Contact David Sibley (toxest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
		Seq primer: -40RP from Gibco.
	FEATURES	Location/Qualifiers
	source	1. .563 /organism="Neospora caninum" /mol_type="mRNA" /db_xref="taxon:29176" /dev_stage="Tachyzoite" /lab_host="GC10 Competent Cells (PGC)" /clone_lib="NC-1 Tachyzoite cDNA Library 2" /note=Vector: Bluescript II SK+; Site: 1: EcoRI; Site 2: XbaI; The cDNA library was constructed by Keliang Tang, and Robert Cole at Washington University. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a XbaI site. Following second strand synthesis, EcoRI adaptors were ligated to the cDNA, and products were size-selected on sephadryl S500. The cDNA were directionally cloned into the EcoRI/XbaI prepared Bluescript II SK+ vector, and electroporated into GC10 Competent Cells (PGC). The library may contain a small percentage of host or bacterial contaminants."
ORIGIN	Query Match	Score 18.6; DB 7; Length 563;
	Best Local Similarity 84.0%; Pred. No. 1.1e+03	Score 18.6; DB 7; Length 563;
	Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Score 18.6; DB 7; Length 563;
FEATURES	Source	
ORIGIN	Location/Qualifiers	
	1. .456 /organism="Toxoplasma gondii" /mol_type="mRNA" /strain="VEG" /db_xref="taxon:5811" /clone="TGESTryza21d01.y1" /dev_stage="Tachyzoite" /lab_host="DH10B" /clone_lib="TGVEG118 Tachyzoite cDNA Library"	
ORIGIN	Query Match	Score 18.6; DB 7; Length 563;
	Best Local Similarity 84.0%; Pred. No. 1.1e+03	Score 18.6; DB 7; Length 563;
	Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Score 18.6; DB 7; Length 563;
FEATURES	Source	
ORIGIN	Location/Qualifiers	
	1. .456 /organism="Toxoplasma gondii" /mol_type="mRNA" /strain="VEG" /db_xref="taxon:5811" /clone="TGESTryza21d01.y1" /dev_stage="Tachyzoite" /lab_host="DH10B" /clone_lib="TGVEG118 Tachyzoite cDNA Library"	
ORIGIN	Query Match	Score 18.6; DB 7; Length 563;
	Best Local Similarity 84.0%; Pred. No. 1.1e+03	Score 18.6; DB 7; Length 563;
	Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Score 18.6; DB 7; Length 563;

Matches	21;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;		
Qy	4	ATGCTGAACCGCAGAGAACCGCG 28									
Db	332	ATGCTGAACGAGAAACGGC 308									
RESULT	25										
ACCESSION	AQ657703	AQ657703	584 bp	DNA	linear	GSS 23-JUN-1999					
DEFINITION		Sheared DNA-21N17.'R Sheared DNA Trypanosoma brucei genomic clone									
VERSION		Sheared DNA-21N17, genomic survey sequence.									
KEYWORDS		AQ657703	GI:516571								
SOURCE	ORGANISM	Trypanosoma brucei									
REFERENCE		Trypanosoma brucei									
AUTHORS		Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.									
TITLE		El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Doneilson,J., Fraser,C. and Adams,M.									
JOURNAL		Determination of clone end sequences from Trypanosoma brucei GUTat 9712									
COMMENT		Unpublished (1999)									
FEATURES	source	Other GSSs: Sheared DNA-21N17.TF									
CLASS		Contact: Najib M. El-Sayed									
LOCATION/QUALIFIERS		Department of Eukaryotic Genomics									
1		The Institute for Genomic Research									
584		9712 Medical Center Dr., Rockville, MD 20850, USA									
5		Tel: 301 838 0200									
0		Fax: 301 838 0208									
0		Email: nel-sayed@tigr.org									
0		Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ARCC. Sheared DNA end sequences search page:									
0		http://www.tigr.org/tdb/mdb/tbdb/ .									
0		Seq primer: M13-Reverse									
0		Class: shotgun.									
0		LOCATION/QUALIFIERS									
0		1									
0		584									
0		/note="Trypanosoma brucei"									
0		/mol type="genomic DNA"									
0		/strain="TREU27/4 GUTat 10.1"									
0		/db_xref="taxon:5691"									
0		/clone="Sheared DNA-21N17"									
0		/clone_lib="Sheared DNA"									
0		NOTE="Vector: PUC18; Site 1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU27/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."									
0		ORIGIN									
0		Query Match	66.4%		Score 18.6;	DB 8;	Length 584;				
0		Best Local Similarity	84.0%		Pred. No. 1.1e+03;						
0		Matches	21;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
0		Qy	1	ATATGCTGAAACCGCGAGAGAACCC 25							
0		Db	12	AAATATCCTGAAACGCCAAATAAACCC 36							
RESULT	26										
LOCUS	FR0021761	FR0021761	593 bp	DNA	linear	GSS 25-FEB-2004					

The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
 Tel: 00 64 09 815 4200
 Fax: 00 64 09 815 4201
 FEATURES
 Email: est@hortresearch.co.nz.
 Location/Qualifiers
 1. .671
 /organism="Malus x domestica"
 /mol_type="mRNA"
 /db_xref="taxon:3750"
 /clone="NASA003156"
 /tissue_type="Young fruit"
 /dev_stage="10 days after full bloom"
 /clone_lib="(AASA) Royal Gala 10 DAFB fruit"
 /note="Vector: pBluescript SK(-); Library sequenced by
 Genesis Research & Development"

ORIGIN
 Query Match 66.4%; Score 18.6; DB 7; Length 671;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 ATATGCTGAAACGGAGAACCG 26
 Db 49 ATATCCTGAAACGGAGAACGAGCTG 73

RESULT 31
 CN879811
 LOCUS CN879811
 DEFINITION 675 bp mRNA linear EST 04-JUN-2004
 domesticica CDNA Clone AASA004412, mRNA sequence.
 ACCESSION CN879811
 VERSION GI:48266051
 KEYWORDS EST.
 SOURCE Malus x domestica (cultivated apple)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Maloideae; Malus.
 REFERENCE 1 (bases 1 to 675)
 AUTHORS Bunning,L., Bowen,J., Crownhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
 TITLE HortResearch Apple EST Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Gleave,A.

Sequencing Facility
 The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
 Tel: 00 64 09 815 4200
 Fax: 00 64 09 815 4201
 FEATURES
 Email: est@hortresearch.co.nz.
 Location/Qualifiers
 1. .675
 /organism="Malus x domestica"
 /mol_type="mRNA"
 /db_xref="taxon:3750"

/clone="NASA004412"
 /tissue_type="Fruit"
 /dev_stage="10 days after full bloom"
 /clone_lib="(AASA) Royal Gala 10 DAFB fruit"
 /note="Vector: pBluescript SK(-); Library sequenced by
 Genesis Research & Development"

ORIGIN
 Query Match 66.4%; Score 18.6; DB 7; Length 675;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 32
 CN918097
 LOCUS CN918097
 DEFINITION 613 bp mRNA linear EST 07-JUN-2004
 ABPB004660HT (ABPB) M9 root tips Malus x domestica cDNA clone
 ACCESSION ABPB004660
 VERSION CN918097
 KEYWORDS EST.
 SOURCE Malus x domestica (cultivated apple)
 ORGANISM Malus x domestica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Maloideae; Malus.
 REFERENCE 1 (bases 1 to 633)
 AUTHORS Bunning,L., Bowen,J., Crownhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
 TITLE HortResearch Apple EST Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Gleave,A.

Sequencing Facility
 The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
 Tel: 00 64 09 815 4200
 Fax: 00 64 09 815 4201
 FEATURES
 Email: est@hortresearch.co.nz.
 Location/Qualifiers
 1. .683
 /organism="Malus x domestica"
 /mol_type="mRNA"
 /db_xref="taxon:3750"
 /clone="ABPB004660"
 /tissue_type="Root tips (distal 1.5 cm)"
 /clone_lib="ABPB" M9 root tips (distal 1.5 cm)"
 /note="Vector: pBluescript SK(-); Library sequenced by
 Genesis Research & Development"

ORIGIN
 Query Match 66.4%; Score 18.6; DB 7; Length 683;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 33
 AQ657387
 LOCUS AQ657387
 DEFINITION Sheared DNA-2N16 TR Sheared DNA Trypanosoma brucei genomic clone
 ACCESSION AQ657387
 VERSION AQ657387.1
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 684)
 AUTHORS El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.
 TITLE Determination of clone end sequences from Trypanosoma brucei GUTAT
 JOURNAL Unpublished (1998)
 COMMENT Other GSSs: Sheared DNA-2N16.TF
 Contact: Najib M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: nelsayed@tigr.org
 Clones are derived from the *Trypanosoma brucei* GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page:
<http://www.tigr.org/tigr/tcdb/mdbs/tbdb/>.
 Seq primer: M13-Reverse
 Class: shotgun.
 Location/Qualifiers
 1. .684
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TRB927/4 GUTat 10.1"
 /db_xref="taxon:1691"
 /clone="Sheared DNA-2N16"
 /clone_lib="Sheared DNA"
 /note_vector: pIC18; Site 1: Small; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TRB927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999).

FEATURES

source

ORIGIN
 Query Match 66.4%; Score 18 6; DB 8; Length 684;
 Best Local Similarity 87.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 AATATGCTAAACGCCAACATAACC 25
 Db 548 AATATCCTAAACGCCAACATAACC 524

RESULT 34
 CL527496 LOCUS CL527496 799 bp DNA linear GSS 11-MAY-2004
 DEFINITION 83k06rp42 f1 RPCI-42 Bos taurus genomic clone 83k06rp42, genomic survey sequence.
 ACCESSION CL527496
 VERSION CL527496.1 GI:47120284
 KEYWORDS
 ORGANISM Bos taurus (cow)
 SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Buteleostomi; Mammalia; Bovidae; Bovine; Bos.
 REFERENCE 1 (bases 1 to 799)
 AUTHORS Aycock, M.M., Najar, L.C., Van Tassel, C.P., Sonstegard, T.S., Conner, E.E., Capucco, A.V. and Roe, B.A.
 TITLE Bovine BAC End Sequences from RPCI-42 Library
 JOURNAL Unpublished (2004)
 COMMENT Contact: Bruce A. Roe
 Advanced Center for Genome Technology
 University of Oklahoma Department of Chemistry and Biochemistry
 620 Parrington Oval, Room 208, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Class: BAC ends
 High quality sequence start: 133
 High quality sequence stop: 524.
 Location/Qualifiers
 1. .799
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="Holstein Bull."
 /db_xref="taxon:913"
 /clone="83k06rp42"
 /sex="male"

/clone lib="RPCI-42"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI"
 ORIGIN
 Query Match 66.4%; Score 18.6; DB 9; Length 799;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 AATATGCTAAACGCCAACATAACC 28
 Db 63 AGTAGNCNGNAACGGAGAAAACCGCG 90

RESULT 35
 CG016439 LOCUS CG016439 427 bp DNA linear GSS 19-AUG-2003
 DEFINITION ZUAG30TH ZM_3.0_4.0_KB Zea mays genomic clone ZMBP0a0006E11, genomic survey sequence.
 ACCESSION CG016439
 VERSION CG016439.1 GI:33888604
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Zea.
 REFERENCE 1 (bases 1 to 427)
 AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budinian, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
 TITLE Consortium for Maize Genomics
 JOURNAL Unpublished (2002)
 COMMENT Other_GSS: ZUAG30TYV
 Contact: Cathy Whitelaw
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: sheared ends.
 Location/Qualifiers 1. .427
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="axon:4577"
 /clone="ZMBP0a0006E11"
 /clone_1ib=ZM_3.0_4.0_KB"
 /note="Vector: pBCK;-Site_1: HincII; 3-4 kb 'unfiltered' genomic DNA library"

ORIGIN
 Query Match 65.7%; Score 18.4; DB 9; Length 427;
 Best Local Similarity 78.6%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AATATGCTAAACGCCAACATAACC 28
 Db 332 AATATGTCACGCTAGAGAGGCCG 359

RESULT 36
 AQ724090 LOCUS AQ724090 456 bp DNA linear GSS 14-JUL-1999
 DEFINITION HS_5375_A2_H09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate_951 Col=18 Row=0, genomic survey sequence.
 ACCESSION AQ724090
 VERSION GSS.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 456)
 Mahaireas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE ID: 99380589
 PUBLMED ID: 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel.: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, Please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Researh Genetics (info@resgen.com). BAC end Web Server:
<http://www.hmsc.washhington.edu>
 Plate: 951 row: O column: 18
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 456.

FEATURES source
 1. .456
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="plate=951 Col=18 Row=O"
 /sex="male"
 /clone.lib="RPCI-11 Human Male BAC Library"
 /clone.id="pBAce3.6"; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAce3.6 vector at EcoRI sites"

ORIGIN
 Query Match 65.7%; Score 18.4; DB 8; Length 456;
 Best Local Similarity 78.6%; Pred. No. 1.3e-03;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGGAGAGAACCGCG 28
 Db 300 ATATGGATTACAGGGTGAAGAACCGCG 273

RESULT 37
 AW599272 LOCUS AW599272 Y1
 DEFINITION 9b12903_Y1 Moss EST library PNP Physcomitrella patens cDNA clone
 PEP SOURCE ID:PPN091205 5', similar to WP:C33F10.3 CE02530 E. COLI
 ORF F226; YEAST YEJ4 PROTEIN ; mRNA sequence.

ACCESSION AW599272.1
 VERSION GI:7286785
 KEYWORDS EST.
 ORGANISM Physcomitrella patens
 Physcomitrella patens
 Bryopsida; Funariales; Funariaceae; Bryophyta; Embryophyta; Bryophytina; Viridiplanteae; Streptophytina; Embryophytina; Embryophyta; Bryophytina; Physcomitrella.
 1 (bases 1 to 456)
 Quatrano,R., Bashirades,S., Cove,D., Cuming,A., Knight,C., Clifton,S., Marrs,M., Hillier,L., Pape,D., Martin,J., Wyllie,T., Underwood,K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Steptoe,M., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
 Unpublished (1999)
 Contact: Ralph Quatrano

Leeds/Wash U Moss EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Libraries were constructed by Dr. Stavros Bashirades as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 416.
 Location/Qualifiers
 1. .496
 /organism="Physcomitrella patens"
 /mol_type="mRNA"
 /db_xref="taxon:3218"
 /clone="PEP SOURCE ID:PPN091205"
 /tissue_type="protonemata"; "7 day old tissue auxin treated"
 /lab_ho="DH10B"
 /clone.lib="Moss EST library PPN"
 /note="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XbaI; Construction of the cDNA library was carried out
 using Stratagene's UniZAP - cDNA synthesis kit."
 /lab_ho="DH10B"
 /note="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XbaI; Construction of the cDNA library was carried out
 using Stratagene's UniZAP - cDNA synthesis kit."
 This cDNA was ligated directionally to a primer/linker that contains
 a XbaI site within it. Following ds cDNA synthesis,
 BcI adapters were ligated to the blunt ends and sample
 was digested with XbaI. The result is cDNA with an EcoRI
 sticky end on one side and a XbaI sticky end on the other.
 This vector was ligated directionally to the blunt ends and on the other.
 vector is designed containing the pBluescript sequence as
 well as lambda DNA and cDNA is cloned within this
 pBluescript sequence. The vector was then packaged using
 Gold Gigapackaging extracts. Library was grown in XLBlue
 MRK™ cells and amplified. The library was excised by mass
 excision using Stratagene's Mass excision kit, that uses
 exonuclease as a helper phage that releases the pBluescript
 sequence and circularizes it as single stranded plasmids
 that are then packaged (by helper phage) and secreted out
 of the host cell as phagemids. SOLR cells were transformed
 with phagemids and the library was plated out on LB-amp
 plates to select for transformants. Approximately
 1,000,000 colonies were grown and recovered. The double
 stranded plasmid library was recovered by using Quiagen
 Midiprep kit. 2 micro grams of each library were used to
 transform DH10B cells by electroporation."

ORIGIN
 Query Match 65.7%; Score 18.4; DB 2; Length 496;
 Best Local Similarity 78.6%; Pred. No. 1.3e-03;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGGAGAGAACCGCG 28
 Db 372 ATTATGGTGAAGGGGAGAAAAAGAG 399

RESULT 38
 BZ130571/c LOCUS BZ130571
 DEFINITION CH230-99416-TU CHORI-230 Segment 2 Rattus norvegicus genomic clone
 CH230-99416, genomic survey sequence
 BZ130571
 ACCESSION BZ130571.1
 VERSION GI:23771518
 KEYWORDS GSS;
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus
 REFERENCE 1 (bases 1 to 582)
 AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsugaya,G., Geer,K.,

JOURNAL Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
COMMENT Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)

Author GSS: CH230-39416.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pjdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or_ering_information.htm). BAC end page: http://www.tigr.org/tgb/bac_ends/rat/bac_end_intro.html

Plate: 394 **row:** I **column:** 6 **Seq primer:** SP6 **Class:** BAC ends.

FEATURES **Source** Location/Qualifiers 1. 582 /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="BN/SsNHsd/MCW" /db_xref="taxon:10116" /clone="CH230-39416" /sex="Female" /cell_type="Brain" /clone_lib="CHORI-230 segment 2" /note=vector: PTARBA1.3; Site 1: MboI; Site 2: MboI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong

ORIGIN Query Match 65.7%; Score 18.4; DB 8; Length 582; Best Local Similarity 78.6%; Pred. No. 1.3e+03; Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT CB020289 CB020289 655 bp mRNA linear EST 10-JAN-2003 LOCUS CB67F07.y1 Haemonchus contortus SL2 TOPO vi Haemonchus DEFINITION contortus cDNA 5' similar to TR:O45812 O45812 T23G11.9 PROTEIN. [1] ORGANISM Haemonchus contortus

REFERENCE McCarter,J., Clifton,S., Chiappelli,B., Pape,D., Martin,J., Wylie,T., Dente,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,R., Bennett,J., Franklin,C., Teagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steck,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
COMMENT Unpublished (1999)
CONTACT: McCarter JP Nematode EST Project, 1999 The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800

JOURNAL Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
COMMENT Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)

Author GSS: CH230-39416.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pjdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.tigr.org/tgb/bac_ends/mouse/bac_end_intro.html)
Plate: 333 **row:** F **column:** 21 **Seq primer:** T7

Fax: 314 286 1810 Email: est@watson.wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL2 PCR based library, CDNA PCR products of size >400 nucleotides containing SL2 on the 5' end and oligo(dT) on the 3', and were non-directionally cloned into pCRII-TOPO (Invitrogen) following the Topo TA protocol. Intestine RNA was provided by Dr. Douglas Jasmer of Washington State University (djasmer@vetmed.wsu.edu).
Seq primer: SL1 primer
 High quality sequence stop: 525.
Location/Qualifiers
 1. .655 /organism="Haemonchus contortus"
 /mol_type="mRNA"
 /db_xref="taxon:6289"
 /feature type="intestine"
 /lab_host="DH10B"
Site 2: EcorI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL2 PCR based library. CDNA PCR products of size >400 nucleotides containing SL2 on the 5' end and oligo(dT) on the 3', and were non-directionally cloned into pCRII-TOPO (Invitrogen) following the Topo TA cloning protocol. Intestine RNA was provided by Dr. Douglas Jasmer of Washington State University (djasmer@vetmed.wsu.edu)."

FEATURES **Source** Location/Qualifiers 1. .655 /organism="Haemonchus contortus"
 /mol_type="mRNA"
 /db_xref="taxon:6289"
 /feature type="intestine"
 /lab_host="DH10B"
Site 1: EcoRI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL2 PCR based library. CDNA PCR products of size >400 nucleotides containing SL2 on the 5' end and oligo(dT) on the 3', and were non-directionally cloned into pCRII-TOPO (Invitrogen) following the Topo TA cloning protocol. Intestine RNA was provided by Dr. Douglas Jasmer of Washington State University (djasmer@vetmed.wsu.edu)."

ORIGIN Query Match 65.7%; Score 18.4; DB 6; Length 655; Best Local Similarity 78.6%; Pred. No. 1.3e+03; Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT BH100535/C BH100535/C LOCUS RPCI-24-333F21-TBV RPCI-24 Mus musculus genomic clone DEFINITION RPCI-24-333F21, genomic survey sequence.
ACCESSION BH100535 VERSION BH100535.1 GI:14924482
KEYWORDS GSS SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthidae; Rodentia; Sciurognathi; Murinae; Mus.
REFERENCE 1 (bases 1 to 672)
AUTHORS Zhao,S., Nierman,W., Malek,J., Sciurognathi; Murinae; Mus.
 Russell,D., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished (1999)
COMMENT Other GSS: RPCI-24-333F21-TBV
CONTACT: Shaying Zhao
Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
VERSION Tel: 301 838 0200
DEFINITION Fax: 301 838 0208
KEYWORDS Email: szhao@tigr.org
ORGANISM Clones may be purchased from BACPAC Resources (http://www.tigr.org/tgb/bac_ends/mouse/bac_end_intro.html)
REFERENCE Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pjdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.tigr.org/tgb/bac_ends/mouse/bac_end_intro.html)
AUTHORS Page: http://www.tigr.org/tgb/bac_ends/mouse/bac_end_intro.html

FEATURES	Class:	BAC ends.	Location/Qualifiers
source	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="RPCI-24-333521"		
	/sex="Male"		
	/cell_type="Spleen/Brain"		
	/clone_lib="RPCI-24"		
	/note="Vector: pTARAC1; Site 1: BamHI; Site 2: BamHI; Site 3: BamHI produced by Piter de Jong. The library was cloned in the pTARAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."		
ORIGIN			
	Query Match	65.7%;	Score 18.4;
	Best Local Similarity	78.6%;	DB 8;
	Matches	22;	Pred. No. 1.3e+03;
	Conservative	0;	Mismatches 0;
			Gaps 0;
Qy	1 AATATGCTGAACGGAGAGAAACCGGG 28		
Db	581 ATTATGCTGAACCTGGAGGAACCTGG 608		
RESULT 42			
	BH929269/c	695 bp	DNA linear
	LOCUS	BH929269	GSS 01-OCT-2002
	DEFINITION	odi81f08_g1_B.oleracea002	Brassica Oleracea genomic, genomic Survey sequence.
	ACCESSION	BH929269	
	VERSION	BH929269_1	GI:23409335
	KEYWORDS	GSS.	
	SOURCE	Brassica oleracea	
	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicots; Spermatophyta; Magnoliophyta; eu dicots; Brassicaceae; Brassica; Brassica oleracea; euroids II; Brassicales; Brassicaceae; Brassica.	
	REFERENCE	1 (bases 1 to 695)	
	AUTHORS	Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.	
	TITLE	Whole Genome Shotgun reads from Brassica oleracea	
	JOURNAL	Unpublished (2002)	
	COMMENT	Contact: Richard K. Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu Plate: odi81 row: f column: 08 Seq primer: -28RPPOT reverse Class: shotgun High quality sequence start: 32 High quality sequence stop: 513. Location/Qualifiers	
	source	1 . 695	
		/organism="Brassica oleracea"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:3172"	
		/clone_lib="B.oleracea002"	
		/note="Vector: pTARAC1; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T0100DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."	
ORIGIN			
	Query Match	65.7%;	Score 18.4;
	Best Local Similarity	78.6%;	DB 8;
	Matches	22;	Pred. No. 1.4e+03;
	Conservative	0;	Mismatches 6;
			Gaps 0;
Qy	1 AATATGCTGAACGGAGAGAAACCGGG 28		
Db	162 AAAATGCCGAAAGGGAGCAAAACCCGG 135		
RESULT 43			
	BH549312/c	697 bp	DNA linear
	LOCUS	BH549312_BOHEP93TR	GSS 14-DEC-2001
	DEFINITION	BOHEP93TR BOHE Brassica oleracea genomic clone BOHEP93, genomic survey sequence.	
	ACCESSION	BH549312	
	VERSION	BH549312_1	GI:17801092
	KEYWORDS	GSS.	

vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public/>"

AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/	source	1. .792
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	/organism="Homo sapiens"	/mol_type="mRNA"
COMMENT	Contact : Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov	/db_xref="taxon:9606"	/clone="IMAGE:5197791"
	Tissue Procurement: CLONETECH Laboratories, Inc.	/lab_host="DH10B"	
	cDNA Library Preparation: CLONETECH Laboratories, Inc.	/clone_lib="NIH MGC_114"	
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIILN)	/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRI (devoid); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRI site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."	
FEATURES	source	ORIGIN	
	1. .790	Query Match	65.7%; Score 18.4; DB 4; Length 792;
	/organism="Homo sapiens"	Best Local Similarity	78.6%; Pred. No. 1.4e+03;
	/mol_type="mRNA"	Matches	Mismatches 6; Indels 0; Gaps 0;
	/db_xref="taxon:9606"		
	/clone="IMAGE:4294639"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/clone_lib="NIH MGC_83"		
	/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: Sfi I (ggccgcctcgcc); Site 2: Sfi I (ggccatratggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGCC-3', and 3' adaptor sequence: 5'-ATTCPAGGGCGAGCGGACATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."		
		RESULT 50	
		BF620613/c	824 bp mRNA linear EST 22-OCT-2001
		LOCUS	HVSMEBC020G05F Hordeum vulgare seedling shoot EST library
		DEFINITION	HVCDA0003 (Etiolated and unstressed) Hordeum vulgare subsp. vulgare cDNA clone HVSMEBC020G05F, mRNA sequence.
		ACCESSION	BF620613.2 GI:13109595
		VERSION	
		KEYWORDS	
		SOURCE	Hordeum vulgare subsp. vulgare
		ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
		REFERENCE	Pooideae; Triticeae; Hordeum.
		AUTHORS	Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begun,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Penton,R.D., Oates,R. and Main,D.
		TITLE	Title for barley genomics: Morex unstressed seedling shoot cDNA library
		JOURNAL	Unpublished (2001)
		COMMENT	On Dec 18, 2000 this sequence version replaced gi:11884347. Contact: Wing RA
		FEATURES	Clemson University Genomics Institute
		source	100 Jordan Hall, Clemson, SC 29634, USA
			Tel: 864 656 7288
			Email: rwing@clemson.edu
			Total hg bases = 279
			Seq primer: ATTAACCCCTACTAAAGCC
			High quality sequence stop: 535.
			Location/Qualifiers
			1. .824
			/organism="Hordeum vulgare subsp. vulgare"
			/mol_type="mRNA"
			/cultivar="Morex"
			/sub_species="vulgare"
			/db_xref="taxon:112509"
			/clone="HVSMEBC0020G05F"
			/tissue type="Seedling shoot"
			/lab_host="JUCI121"
			/clone_lib="Hordeum vulgare seedling shoot EST library HVCDA0003 (Etiolated and unstressed)"
			/note="Vector: lambdaAP; Site_1: EcoR1; Site_2: Xhol; Seeds were surface sterilized then germinated under axenic
		FEATURES	
		source	

conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were *in vivo* excised to give pBluecript SK(-) cDNA phagemids. These steps were performed in the FU Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begin, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Ranbo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders>. Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggbpages/bgn/31/cover.html>)

ORIGIN

	Query Match	Score	Length
Best	Local Similarity	18.4;	824;
Matches	22; Conservative	DB 2;	
Qy	1 AAATATGCTGAAACGCCAGAGAAAACCCGG	No. 1.4e+03;	
Db	821 AATAAAGCGAAAGAGAGAGAAAACCGAG	Mismatches 0;	
		Indels 6;	
		Gaps 0;	

1 AAATATGCTGAAACGCCAGAGAAAACCCGG 28
821 AATAAAGCGAAAGAGAGAGAAAACCGAG 794

Search completed: January 19, 2005, 13:54:06
Job time : 1555 secs

THIS PAGE BLANK (USPTO)